

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 13:14:58 ; Search time 56 Seconds
 Perfect score: 754 (without alignments)
 Sequence: 1 MAMVSAWSWLYLWISACM.....SGWCATGKIKTRIHPRT 133

Title: US-09-763-335-2
 Scoring table: BLOSUM62
 Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: _geneseqP1980s:*
- 2: _geneseqP1990s:*
- 3: _geneseqP2000s:*
- 4: _geneseqP2001s:*
- 5: _geneseqP2002s:*
- 6: _geneseqP2003as:*
- 7: _geneseqP2003bs:*
- 8: _geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	754	100.0	133	3	AAY70400	Aay70400 Human cel
2	754	100.0	133	4	AAM78667	Aam78667 Human Pro
3	754	100.0	190	4	AAM79651	Aam79651 Human Pro
4	746	98.9	133	4	ABU52838	Abu52838 Human kid
5	432	57.3	131	4	AAM39191	Aam39191 Human kid
6	432	57.3	242	4	AAM40977	Aam40977 Human Pro
7	241	32.0	121	3	AAB44958	Aab44958 Human sec
8	241	32.0	132	3	AAY53016	Aay53016 Human sec
9	240.5	31.9	89	4	ABU52839	Abu52839 Human kid
10	221.5	29.4	115	4	AAM24360	Aam24360 Human EST
11	150	19.9	29	2	AAY13167	Aay13167 Human sec
12	110.5	14.7	120.2	7	ADB60833	Ade60833 Rat Prote
13	96	12.7	1984	2	Aaw95557	Aaw95557 Mus muscu
14	95.5	12.7	2331	7	ADB63713	Ade63713 Rat Prote
15	95.5	12.7	2531	7	ADB63705	Ade63705 Rat Prote
16	17	12.7	2531	7	ADB63709	Ade63709 Rat Prote
17	95.5	12.7	2331	7	ADB63701	Ade63701 Rat Prote
18	92.5	12.3	2146	4	ABB62317	Abb62317 Drosophil
19	91.5	12.1	233	2	AAY29053	Aay29053 T. gondii
20	91.5	12.1	233	2	AAB2524	Aab2524 T. gondii
21	87	11.5	188	4	AAU8112	Aau8112 Novel hum
22	87	11.5	188	4	AAT17021	Aat17021 Human nov
23	87	11.5	188	4	AB10465	Ab10465 Human CDN
24	87	11.5	188	4	AAU19912	Aau19912 Novel hum
25	87	11.5	188	5	Abj05739	Abj05739 Novel hum

RESULT 1
 ID AAY70400 standard; protein; 133 AA.

XX AAY70400;
 XX AC
 DT 21-JUN-2000 (first entry)

DE Human cell-signalling protein-2.

KW Human cell-signalling protein-2; neoplastic disorder; smooth muscle disorder; vesicle trafficking disorder; asthma; emphysema; rheumatoid arthritis;

KW HIV; human immunodeficiency virus; osteoporosis; multiple sclerosis;

KW artherosclerosis; diabetes mellitus; psoriasis; viral infection;

KW irritable bowel syndrome; bacterial infection; fungal infection;

KW cytotoxic; antiarthritic; antidiabetic; immunosuppressive;

KW antiarrhythmic; claretic; anti-HIV; antipsoriatic; antiflammatory;

KW neuroprotective; antipsoriatic; antimicrobial; drug screening.

XX Homo sapiens.

OS Homo sapiens.

XX

XX Key Peptide

XX Location/Qualifiers 1..25 /label= Signal_peptide

XX FT 64 /note= "Protein kinase C phosphorylation site"

XX FT Modified-site 77 /note= "Protein kinase C phosphorylation site"

XX FT Modified-site 83 /note= "Casein kinase II phosphorylation site"

XX FT Modified-site 109 /note= "Casein kinase II phosphorylation site"

XX FT Modified-site 126 /note= "Protein kinase C phosphorylation site"

XX WO200011169-A2.

XX PD 02-MAR-2000.

XX FT 19-AUG-1999; 99WO-US019072.

XX PR 21-AUG-1998; 98US-0013757B.

XX PR (INCY-) INCYTE PHARM INC.

PI Tang YT, Corley NC, Patterson C, Guegler KJ, Baughn MR,

ALIGNMENTS

XX WPI; 2000-246562/21.
DR N PSDB; AA51528.
XX New human cell signaling proteins and polymucleotides useful for diagnosis, prevention and treatment of neoplastic, neurological, immunological, vesicle trafficking and smooth muscle disorders.
XX PT PT
XX PS Claim 1; Page 60; 62pp; English.

CC The present sequence is human cell-signalling protein-2 (CSIG-2) involved in regulation of cell proliferation, differentiation and gene transcription. CSIG can be used in the diagnosis and treatment of diseases associated with expression of CSIG. These diseases include neoplastic, neurological, immunological, vesicle trafficking and smooth muscle disorders, including HIV, rheumatoid arthritis, asthma, arterioclerosis, diabetes mellitus, emphysema, irritable bowel syndrome, multiple sclerosis, osteoporosis, psoriasis and infections including viral, bacterial and fungal. CSIG and its catalytic or immunogenic fragments are useful for drug screening using libraries of compounds

XX Sequence 133 AA;

Query Match Score 754; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.9e-6;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMYSAMSWLYLWISACMLLCHGSQHTFQQLHLRPEGGTCEVAAHRCNNKRLEE 60
Db 1 MAMYSAMSWLYLWISACMLLCHGSQHTFQQLHLRPEGGTCEVAAHRCNNKRLEE 60
Qy 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Db 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Qy 121 GNKIKTRIHPRT 133
Db 121 GNKIKTRIHPRT 133
Db 121 GNKIKTRIHPRT 133

RESULT 2
ID AAM78667 standard; protein; 133 AA.
XX AAM78667;
AC AC

XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 1329.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PP 05-FEB-2001; 2001WO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00568075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX PA (HYSEQ INC.)

XX PI Tang YT, Liu C, Dumanac RT, Asundi V, Zhou P, Xu C, Cao Y; Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wehrman T, Goodrich R; DR N-PSDB; AA51800.
XX PS Nucleic acids encoding polypeptides with cytokine-like activities, useful for diagnosis and gene therapy.

XX Claim 20; Page 3574; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM878323-AAM8302) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematoopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM8020) are omitted as the relevant pages from the sequence listing were missing at the time of publication

XX SQ Sequence 133 AA;

Query Match Score 754; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.9e-6;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMVSAMSWLYLWISACMLLCHGSQHTFQQLHLRPEGGTCEVAAHRCNNKRLEE 60
Db 1 MAMVSAMSWLYLWISACMLLCHGSQHTFQQLHLRPEGGTCEVAAHRCNNKRLEE 60
Qy 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Db 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Qy 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Db 61 RSQTIVKCSCLPGKVAGTPRNPSCVDASTIVGRKWCEMPCLGECKTLPDNSGMCAT 120
Qy 121 GNKIKTRIHPRT 133
Db 121 GNKIKTRIHPRT 133

RESULT 3
ID AAM79651
XX DE AAM79651 standard; protein; 190 AA.
AC AC

XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3297.
XX KW Human cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematoopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PP 05-FEB-2001; 2001WO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00568075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX PA (HYSEQ INC.)

Page 3

PR 19-JUL-2000; 2000US0-00620312.
 PR 03-AUG-2000; 2000US0-0053450.
 PR 14-SEP-2000; 2000US0-00662191.
 PR 19-OCT-2000; 2000US0-00693036.
 XX 29-NOV-2000; 2000US0-00727344.
 PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;
 XX DR WPI; 2001-442253/47.
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
 XX PS Example 4; SEQ ID NO 2336; 1070pp; English.
 XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AM38642-AM42213) with nootropic, immunosuppressant and cytosstatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemoattractant/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CNS disorders. Note: The sequence data for this patent did not form part of the printed specification
 XX SQ Sequence 131 AA;
 Query Match 57.3%; Score 432; DB 4; Length 131;
 Best Local Similarity 61.2%; Pred. No. 2e-36;
 Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;
 Qy 9 WVLYLWISACAMLCHGSLQHTEQQHHLHRPSEGTCBVIAAHRCCNKRIBERSQTVKCS 68
 Db 19 FIVTLW-----GKVSSANHHKAHHVKTGTCEVVAHRCCNKRIBERSQTVKCS 68
 Qy 69 CLPGKVAGTTRNPSPCDVASIVIGKWWCEMPELEGEBCKLDPNSGWMCATGNKIKTTR 128
 Db 69 CFPGQVAGTTRAPSCVDASIVEQKWNCHMMPQLEGECKLDPDKGMWSGGNKNVKITTR 128
 Qy 129 I 129 :
 Db 129 V 129 ;
 RESULT 6
 ID AAB44957
 XX AAB44977 standard; protein; 242 AA.
 AC AAB44977;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 5908.
 XX KW Human; nootropic; immunosuppressant; cytosstatic; gene therapy; cancer; peripheral nervous system; neuropathy; huntington's disease; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; myotrophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
 XX OS Homo sapiens.

XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US034263.
 XX PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-0048825.
 PR 25-APR-2000; 2000US-0055217.
 PR 20-JUN-2000; 2000US-0059842.
 PR 19-JUL-2000; 2000US-0062012.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-0066291.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 XX DR N-PSDB; AA160133.
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
 XX Example 2; SEQ ID NO 5908; 1007pp; English.
 XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AM38642-AM42213) with nootropic, immunosuppressant and cytosstatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activation/inhibin activity, chemokinetic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CNS disorders. Note: The sequence data for this patent did not form part of the printed specification
 XX SQ Sequence 242 AA;
 Query Match 57.3%; Score 432; DB 4; Length 242;
 Best Local Similarity 61.2%; Pred. No. 3.9e-36;
 Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;
 Qy 9 WVLYLWISACAMLCHGSLQHTEQQHHLHRPSEGTCBVIAAHRCCNKRIBERSQTVKCS 68
 Db 130 FIVTLW-----GKVSSANHHKAHHVKTGTCEVVAHRCCNKRIBERSQTVKCS 179
 Qy 69 CLPGKVAGTTRNPSPCDVASIVIGKWWCEMPELEGEBCKLDPNSGWMCATGNKIKTTR 128
 Db 180 CFPGQVAGTTRAPSCVDASIVEQKWNCHMMPQLEGECKLDPDKGMWSGGNKNVKITTR 239
 Qy 129 I 129 :
 Db 240 V 240 ;
 RESULT 7
 ID AAB44958
 XX AAB44958 standard; protein; 121 AA.
 AC AAB44958;
 XX DT 12-FEB-2001 (first entry)

QY	6 AMNSWLYLWISACAMLLCHGSIQLHTFQOHHLHRPEGOTCEVAAHRCNNKNRTEERSVQ 65
DB	6 SMMSTWAFMILASITYAC5-----QLAAGTCIVILDRDSSQPRRTAROTA 54
QY	66 KCSCSFLGKVGATGTRNPSCVDASIVIGKWWCMEPCLEGECKTLPDNSGMMCP-TGNK1 124
DB	55 RCACRKGQIAGTTRARPACVDARIKTKQWCIDMLPCLGEGCDDILINRSGWTCQPGR1 114
QY	125 KTTTR 129
DB	115 KTTTV 119
	RESULT 8
	AAV53016
ID	AAV53016 standard; protein; 132 AA.
XX	
AC	AAV53016;
XX	
DT	29-FEB-2000 (first entry)
XX	
DE	Human secreted protein clone ml243_1 protein sequence SEQ ID NO:38.
XX	
KW	Human; secreted protein; nutritional; cytokine; cell proliferation;
KW	differentiation; immune stimulating; vaccine; suppression; inhibin; chemotactic;
KW	haemopoiesis; regulation; tissue growth; activin; inhibin; chemotactic;
KW	hemokinetic; haemostatic; thrombolytic; receptor; ligand;
KW	anti-inflammatory; cadherin; tumour invasion suppressor;
KW	tumour inhibition; gene therapy.
XX	
OS	Homo sapiens
XX	
PN	WO957132-A1.
XX	
PD	11-NOV-1999.
XX	
PF	99WO-US00970.
XX	
PR	07-MAY-1998; 9B0US-0084564P.
PR	09B0US-0084564P.
PR	22-JUL-1998; 9B0US-0093112P.
PR	31-JUL-1998; 9B0US-0094935P.
PR	10-AUG-1998; 9B0US-0094980P.
PR	11-AUG-1998; 9B0US-0096068P.
PR	06-MAY-1999; 99US-00306111.
XX	
(GENRY) GENETICS INST INC.	
JACOBS K, MCCOY JM, LAVALLIE ER, COLLINS-RACIE LA, EVANS C;	
PI	MERBERG D, TRACY M, AGOSTINO MJ, STAININGER RJ, BOWMAN MR;
PI	DIBLASSIO-SMITH E, WIDDOW A;
DR	WPI: 2000-052937/04.
DR	N-PSDB: AAZ333334.
XX	New polynucleotides encoding secreted human proteins, derived from adult
PT	placenta, adult retina, fetal brain.
XX	Claim 47; Page 397: 492pp; English.
PS	The present invention describes new human secreted proteins which were
CC	isolated from adult placenta, adult retina, foetal brain, foetal kidney,
CC	adult blood, adult brain, adult thyroid, adult neural
CC	tissue, adult testes, and adult lymph node cDNA libraries. The human
CC	secreted proteins, and the polynucleotides encoding them, are predicted
CC	to have biological activities which would make them suitable for
CC	treating, preventing or ameliorating medical conditions in humans and
CC	animals. Suggested activities include nutritional activity, cytokine and
CC	cell proliferation/differentiation, haemopoiesis regulating activity,
CC	vaccine or suppressing activity, haemostatic and thrombolytic activity,
CC	chemotactic/chemokinetic activity, activin/inhibin activity,
CC	anti-inflammation activity, cationic tumour
SQ	Sequence 121 AA;
SQ	Score 241; DB 3; Length 121;
Query Match	32.0%
Best Local Similarity	38.4%
Matches	Pred. No. 7 2e-17; Mismatches 23; Conservatve 42;
	Gaps 12; Gaps 2;

CC invasion suppressor activity, and tumour inhibition activity. The
 CC polynucleotides are also stated to be useful for gene therapy; AA233316
 CC to AA233373 encode human secreted proteins, and AI5398 to AY53060
 CC represent human secreted proteins, given in the present invention
 XX Sequence 132 AA;

Query Match 32.0%; Score 241; DB 3; Length 132;
 Best Local Similarity 38.4%; Pred. No. 7.9e-17;
 Matches 48; Conservative 23; Mismatches 42; Indels 12; Gaps 2;

Qy 6 AMSVLYLWISACAMLICHLGSSLQHTFQQHHHLHREGGTCEVIAHRCNCNKRTEERQTV 65

Db 18 SMSSTFWAMILASILIAVCS-----QLAAGTCIVILDRDSQSPRTIAQTA 66

Qy 66 KCSCSLPGKXAGTTRNPRSCVDASIVIGKWCENPCLGECKTLPDNSGWMCA-TGNKI 124

Db 67 RCACRKQQTATGTRAPCVDARIKTKWCDMPLPCLEGEQGCDLLINRSGWICTOPGGR 126

Qy 125 KITRI 129

Db 127 KITTY 131

RESULT 9

ABU52839 standard; protein: 89 AA.

XX AC ABU52839;

XX DT 14-APR-2003 (first entry)

XX DE Human kidney derived protein DKFZPhEkd2_4b6 homologue.

XX Human; gene therapy; vaccine; disease treatment; detection.

XX Homo sapiens.

XX EN W0200112659-A2.

XX PD 22-FEB-2001.

XX PP 18-AUG-2000; 2000WO-1B001496.

XX PR 18-AUG-1999; 99US-0149499P.

XX PR 28-SEP-1999; 99US-0156503P.

XX PA (GBHU-) GERMAN HUMAN GENOME PROJECT.

XX PI Wiemann S;

XX DR WPI; 2001-327840/34.

XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies.

XX Example III; Page 426; 1035pp; English.

CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence represents a homologue
 CC of a polypeptide described in the disclosure of the invention
 XX Sequence 89 AA;

Query Match 31.9%; Score 240.5; DB 4; Length 89;
 Best Local Similarity 49.4%; Pred. No. 5.7e-17;

CC invasion suppressor activity, and tumour inhibition activity. The
 CC polynucleotides are also stated to be useful for gene therapy; AA233316
 CC to AA233373 encode human secreted proteins, and AI5398 to AY53060
 CC represent human secreted proteins, given in the present invention
 XX Sequence 132 AA;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Matches 48; Conservative 23; Mismatches 42; Indels 12; Gaps 2;

Qy 6 AMSVLYLWISACAMLICHLGSSLQHTFQQHHHLHREGGTCEVIAHRCNCNKRTEERQTV 65

Db 18 SMSSTFWAMILASILIAVCS-----QLAAGTCIVILDRDSQSPRTIAQTA 66

Qy 66 KCSCSLPGKXAGTTRNPRSCVDASIVIGKWCENPCLGECKTLPDNSGWMCA-TGNKI 124

Db 67 RCACRKQQTATGTRAPCVDARIKTKWCDMPLPCLEGEQGCDLLINRSGWICTOPGGR 126

Qy 125 KITRI 129

Db 127 KITTY 131

RESULT 9

ABU52839 standard; protein: 115 AA.

XX ID AAM24360 standard; protein: 115 AA.

XX ID AAM24360 standard; protein: 115 AA.

XX AC AAM24360;

XX DT 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1885.

XX DE Human EST encoded protein SEQ ID NO: 1885.

XX Human; sheep; pig; cow; fruit fly; yeast; macaque; horse;

XX Human; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; Gene mapping; genetic disorder; biodiversity;

XX gene therapy; nutrition.

XX OS Homo sapiens.

XX PN WO200154477-A2.

XX PD 02-AUG-2001.

XX DE 25-JUN-2001; 2001WO-US002687.

XX PR 25-JAN-2000; 2000US-00491404.

XX PR 17-JUL-2000; 2000US-00631746.

XX PR 03-AUG-2000; 2000US-00631451.

XX PR 15-SEP-2000; 2000US-00663870.

XX PA (HYSE) HYSE INC.

XX PR Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX PI Cao Y, Drmanac RA, Zhang J, Wehrman T;

XX XX DR WPI; 2001-476164/51.

XX DR N-PSDB; AAH99019.

XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use.

XX PS Claim 20; Page 1217-1218; 1275pp; English.

XX CC The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

XX protein of the invention

XX Sequence 115 AA;

XX XX XX

XX XX XX

XX XX XX

XX XX PR

XX PR 18-AUG-1999;

XX PR 28-SEP-1999;

XX PA 99US-0156503P.

XX PA (GBHU-) GERMAN HUMAN GENOME PROJECT.

XX PI Wiemann S;

XX DR WPI; 2001-327840/34.

XX PT Nucleic acids having the sequences of clones isolated from libraries of

PT different human tissues, useful in recombinant DNA methodologies.

XX PS Example III; Page 426; 1035pp; English.

CC This invention describes novel polynucleotides and polypeptides isolated

CC from human cDNA libraries which can be used for gene therapy or in

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate polypeptide expression. The products of the

CC invention may also be used to identify modulators of expression and

CC activity and to down regulate expression and activity. The antibodies of

CC the invention may also be used as diagnostic agents for detecting the

CC presence of polypeptides in samples. This sequence represents a homologue

CC of a polypeptide described in the disclosure of the invention

XX Sequence 89 AA;

XX XX XX

XX XX XX

XX XX PR

XX PR 18-AUG-1999;

XX PR 28-SEP-1999;

XX PA 99US-0156503P.

XX PA (GBHU-) GERMAN HUMAN GENOME PROJECT.

XX PI Wiemann S;

XX DR WPI; 2001-327840/34.

CC Nucleic acids having the sequences of clones isolated from libraries of

PT different human tissues, useful in recombinant DNA methodologies.

XX PS Example III; Page 426; 1035pp; English.

CC This invention describes novel polynucleotides and polypeptides isolated

CC from human cDNA libraries which can be used for gene therapy or in

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate polypeptide expression. The products of the

CC invention may also be used to identify modulators of expression and

CC activity and to down regulate expression and activity. The antibodies of

CC the invention may also be used as diagnostic agents for detecting the

CC presence of polypeptides in samples. This sequence represents a homologue

CC of a polypeptide described in the disclosure of the invention

XX Sequence 89 AA;

XX XX XX

CC Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

CC Nucleic acids having the sequences of clones isolated from libraries of

PT different human tissues, useful in recombinant DNA methodologies.

XX PS Example III; Page 426; 1035pp; English.

CC This invention describes novel polynucleotides and polypeptides isolated

CC from human cDNA libraries which can be used for gene therapy or in

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate polypeptide expression. The products of the

CC invention may also be used to identify modulators of expression and

CC activity and to down regulate expression and activity. The antibodies of

CC the invention may also be used as diagnostic agents for detecting the

CC presence of polypeptides in samples. This sequence represents a homologue

CC of a polypeptide described in the disclosure of the invention

XX Sequence 89 AA;

XX XX XX

CC Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

CC Nucleic acids having the sequences of clones isolated from libraries of

PT different human tissues, useful in recombinant DNA methodologies.

XX PS Example III; Page 426; 1035pp; English.

CC This invention describes novel polynucleotides and polypeptides isolated

CC from human cDNA libraries which can be used for gene therapy or in

CC them may be used in the prevention, diagnosis and treatment of diseases

CC associated with inappropriate polypeptide expression. The products of the

CC invention may also be used to identify modulators of expression and

CC activity and to down regulate expression and activity. The antibodies of

CC the invention may also be used as diagnostic agents for detecting the

CC presence of polypeptides in samples. This sequence represents a homologue

CC of a polypeptide described in the disclosure of the invention

XX Sequence 89 AA;

XX XX XX

CC Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Best Local Similarity 38.4%; Pred. No. 7.9e-17;

Query Match 31.9%; Score 240.5; DB 4; Length 89;

Best Local Similarity 49.4%; Pred. No. 5.7e-17;

Query Match 32.0%; Score 241; DB 3; Length 132;

Db 62 ERSQTVKGSFCQQVAGTTRAKPSCVD 88

RESULT 11
 AAY13167
 ID AAY13167 standard; protein; 29 AA.
 XX
 AC AAY13167;
 XX DT 22-JUN-1999 (first entry)
 XX DE Human secreted protein encoded by 5' EST SEQ ID NO: 181.
 XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 upstream regulatory sequence; cytokine activity; cell proliferation;
 differentiation; haemopoiesis regulation; tissue growth regulation;
 reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 thrombolytic; anti-inflammatory; tumour inhibition.
 XX OS Homo sapiens.
 XX PN WO9906552-A2.
 XX PD 11-FEB-1999.
 XX PP 31-JUL-1999;
 PR 01-AUG-1997;
 PA (GEST) GENSET.
 PI Dumas Milne Edwards J, Ducleurt A, Lacroix B;
 XX WPI; 1999-153782/13.
 DR N-PSDB; AAX51967.
 XX PT New isolated brain-derived nucleic acids - used to develop products which
 PT may have cytokine, immune, regulatory, haematopoiesis regulating, anti-
 inflammatory or tumour inhibition activity.
 PS Claim 34; Page 548; 577pp; English.
 XX AAX51787 to AAX52019 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12987 to
 CC AAY13219, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensics, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell
 XX Sequence 29 AA;

Query Match 19.9%; Score 150; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.2e-08;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MAMVSAMSWSWLYIWISACMMLCHGSIQ 28
 1 MAMVSAMSWSWLYIWISACMMLCHGSIQ 28

RESULT 12

Query Match 14.7%; Score 110.5; DB 7; Length 1202;
 Best Local Similarity 27.0%; Pred. No. 0.022;
 Matches 33; Conservative 13; Mismatches 27; Indels 49; Gaps 9;

CNKNRI- 58 : : : |

Db 419 CHGQCOH-----GGTCKDLVNGYQCVCPRGGRHCELEYKCASSPCRRGGIC 467
 Qy 59 EERSQITKCSCLPGKTYAGTTRNRPSC-VDASIVIGRWCEMEPCLGEBCCTLPDNSGWM 117
 :
 Db 468 EDLVDFRCHC-PRGLSG----PLCEVDVDL---WCEPNPCLNGARCYNLLEDD--YY 514
 Qy 118 CA 119
 Db 515 CA 516

RESULT 13
 ID AAW95557 standard; protein; 1964 AA.
 XX AC AAW95557;
 XX DT 16-JUN-1999 (first entry)
 XX DE Mus musculus notch4 protein.
 XX KW notch4; int-3; antisense; angiogenesis; modulation; inhibition;
 KW promotion; solid tumour; haemangioma; haemangiosarcoma; Kaposi's sarcoma;
 KW ischaemia; gangrene; treatment; hemangioma; diabetic ulcers;
 KW chronic ulceration; hemangiosarcoma;
 KW cerebral autosomal dominant arteriopathy; subcortical infarction;
 KW leucoencephalopathy; vascular dementia; wound healing.

OS Mus musculus.
 XX Key Location/Qualifiers
 FT Region 804 .806 /note= "putative glycosylation site"
 FT Region 1139 .1141 /note= "putative glycosylation site"
 FT Region 1411 /note= "int-3 oncoprotein initiating Methionine"
 FT Domain 1441 .1164 /note= "transmembrane domain"
 FT Domain 1925 .1941 /note= "putative PEST domain"
 FT WO9857621-A1.
 XX PD 23-DEC-1998.
 XX PF 18-JUN-1998; 98WO-US013050.
 PR 18-JUN-1997; 97US-00878351.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Kitajewski, J; Uttenraad, H;
 DR WPI; 1999-095286/08.
 XX N-PSDB; AXX00989.

PT New nucleic acid encoding Notch4 Protein - used to modulate angiogenesis,
 PT e.g. for treatment of tumours, ischaemia, ulcers and wounds
 XX PS Claim 5; Fig 1; 118pp; English.

CC The sequence is that of the notch4 protein. Antibodies (Ab) raised
 CC against it are used to block binding of notch4 protein to its ligand.
 CC Agonists and antagonists are used to modulate (promote or inhibit,
 CC respectively) angiogenesis; this is also promoted by transducing cells to
 CC express notch4, and optionally its ligand, or inhibited by treatment with
 CC Ab, or their fragments. Specifically inhibition of angiogenesis is used
 CC to treat solid tumours, haemangiomas, haemangiosarcoma and Kaposi's
 CC sarcoma, while its promotion is used to treat ischaemia, gangrene,
 CC diabetic ulcers, chronic ulceration, cerebral, atherosomal, dominant
 CC arteriopathy with subcortical infarcts and leucoencephalopathy, vascular
 CC dementia and wounds. Ab are also used to detect notch4 protein on the

CC surface of cells. Signalling through notch4: (a) is distinct from that
 CC through fibroblast growth factor (FGF), so may effect angiogenesis not
 CC responsive to FGF modulation; (b) determines the fate of a cell, so is
 CC effective in presence of other angiogenic factors, and (c) may show a
 CC synergistic effect with FGF signalling
 XX SQ Sequence 1964 AA;

Query Match 12.7%; Score 96; DB 2; Length 1964;
 Best Local Similarity 26.8%; Pred. No. 1.2;
 Matches 33; Conservative 8; Mismatches 48; Indels 34; Gaps 6;

Qy 15 ISACAMLLC-HGSLOHTFQQHHLHRPEGGTC-----EVIAAHR--CCNKRI 58
 DB 689 LGGCSTPCAGGTCP-----QFSGYNTCPAGMGTCSERVATCNSGPCLNGGSC 741
 Qy 59 EERSQTVKCSCLPGKTYAGTTRNRPSCDASIVIGKWWCMEPCLGECECKLTPDNSGWC 118
 DB 742 SIRPREGYSCTLP-----SHTGRHCCQTAVD-----HCVSASCLNGGTCVNKPGTFFCLC 790
 Qy 119 ATG 121
 DB 791 ATG 793

RESULT 14
 ID ADE63713 standard; protein; 2531 AA.
 XX AC ADE63713;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein CRA40667, SEQ ID NO 9657.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNL; Chung.
 XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002NO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX PA (GERHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX PI Woolf, C; D'urso, D; Befort, K; Costigan, M;
 XX DR WPI; 2003-268312/26.
 XX GENBANK; CAA40667.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially expressed in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the Printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 2531 AA;

Query Match Score 95.5; DB 7; Length 2531;
Best Local Similarity 12.7%; Pred. No. 1.7;
Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;Qy 15 ISACAMILGSLOHTFQOHHLHRPEGGTCE-VIAAHC-----ONRN 56
Db 679 IDECAGSPH-----NGTCTEDIAGFTCRCPGYHDPTCLSVNECNNS 723
Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 111
Db 724 PCIHGACRDGLNGYKCDAPG-WSGTNCD-----INNNECESNPONGTCKDM- 771
Qy 112 DNGWMC 118
Db 772 -TSGYVC 777

RESULT 15
 ID ADB63705 standard; protein; 2531 AA.
 XX ADB63705;
 AC :
 DT 29-JAN-2004 (first entry)
 XX DE Rat Protein CAA40667, SEQ ID NO 9649.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2003WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

PA (GERHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX PI Woolf, C, D'urso, D, Befort, K, Costigan, M;
 XX DR WPI; 2003-268312/26.
 DR GENBANK, CA00667.

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XX Claim 1; Page; 1017pp; English.

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 CC or human polynucleotides or a polynucleotide which represents a fragment,
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 CC claimed are a vector comprising the novel polynucleotide, a host cell
 comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the Printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

XX SQ Sequence 2531 AA;
 Query Match Score 95.5; DB 7; Length 2531;
 Best Local Similarity 12.7%; Pred. No. 1.7;
 Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

Qy 15 ISACAMILGSLOHTFQOHHLHRPEGGTCE-VIAAHC-----ONRN 56
 Db 679 IDECAGSPH-----NGTCTEDIAGFTCRCPGYHDPTCLSVNECNNS 723
 Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 118
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 Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

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 Db 679 IDECAGSPH-----NGTCTEDIAGFTCRCPGYHDPTCLSVNECNNS 723
 Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 111
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 Best Local Similarity 12.7%; Pred. No. 1.7;
 Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

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 Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 118
 Db 724 PCIHGACRDGLNGYKCDAPG-WSGTNCD-----INNNECESNPONGTCKDM- 777
 XX SQ Sequence 2531 AA;
 Query Match Score 95.5; DB 7; Length 2531;
 Best Local Similarity 12.7%; Pred. No. 1.7;
 Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

Qy 15 ISACAMILGSLOHTFQOHHLHRPEGGTCE-VIAAHC-----ONRN 56
 Db 679 IDECAGSPH-----NGTCTEDIAGFTCRCPGYHDPTCLSVNECNNS 723
 Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 111
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 XX SQ Sequence 2531 AA;
 Query Match Score 95.5; DB 7; Length 2531;
 Best Local Similarity 12.7%; Pred. No. 1.7;
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Qy 15 ISACAMILGSLOHTFQOHHLHRPEGGTCE-VIAAHC-----ONRN 56
 Db 679 IDECAGSPH-----NGTCTEDIAGFTCRCPGYHDPTCLSVNECNNS 723
 Qy 57 ----RIEERSQTVKCSCLPGLKYGHTPRNPSCVDAASIVGKWCMEPLGECKTL 118
 Db 772 -TSGYVC 777

Result No.	Score	Query Match Length	DB ID	Description
1	11.0	14.7	JAG2_RAT	P97607 rattus norvegicus
2	9.6	12.7	NTC4_MOUSE	P31695 mus musculus
3	9.5	12.7	NTCL_RAT	Q01705 mus musculus
4	9.5	12.7	NTCL_RAT	Q01708 rattus norvegicus
5	9.2	12.3	CRB_DROME	P10040 drosophila
6	9.1	12.1	JAG3_BRARE	Q9Y54 brachydanio
7	9.1	12.1	DIP87_DICDI	Q04503 dictyostelia
8	8.6	11.5	NOTC_DROME	P07207 drosophila
9	8.6	11.4	685	JAG1_HUMAN
10	8.6	11.4	1218	JAG1_MOUSE
11	8.6	11.4	1218	JAG1_MOUSE
12	8.5	11.4	1219	JAG1_RAT
13	8.5	11.3	1064	FBP1_STRPDU
14	8.4	11.2	2003	NTC4_HUMAN
15	8.4	11.1	1247	JAG2_MOUSE
16	8.4	11.1	2524	JAG2_XENLA
17	8.3	11.1	1170	TSP2_BOVIN
18	8.2	10.9	2470	NTC2_MOUSE
19	8.2	10.9	2471	NTC2_HUMAN
20	8.2	10.9	2471	NTC2_RAT
21	8.2	10.9	2318	NTC3_MOUSE
22	8.2	10.9	4544	JAG1_HUMAN
23	8.2	10.9	5376	ZAN_MOUSE
24	8.1	10.8	355	YMT5_YEAST
25	8.1	10.8	2556	NTC1_HUMAN
26	8.0	10.7	2321	NTC3_HUMAN
27	8.0	10.6	937	VME_BOVIN
28	7.9	10.5	2319	NTC3_RAT
29	7.9	10.5	819	AD09_HUMAN
30	7.8	10.4	1178	TSP2_CHICK
31	7.8	10.4	3312	CLR3_HUMAN
32	7.8	10.3	1191	LRG2_MOUSE
33	7.8	10.3	1376	CRBH_HUMAN
				Q35516 mus musculus
				Q40418 saccharomyces_cerevisiae
				P04721 homo sapiens
				Q9TWW3 rattus norvegicus
				Q61982 mus musculus
				Q07954 homo sapiens
				Q88799 mus musculus
				Q40418 saccharomyces_cerevisiae
				P46531 homo sapiens
				Q9um47 homo sapiens
				P80012 bos taurus
				Q9r172 rattus norvegicus
				Q13443 homo sapiens
				P35440 gallus gallus
				Q9nyq7 homo sapiens
				Q61092 mus musculus
				P82279 homo sapiens

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

%

SUMMARIES

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

JAG2_RAT

ID: JAG2_RAT

STANDARD;

PRT; 1202 AA.

AC P97607;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 41, Last annotation update)

DE Jagged2 (Jagged2) (Fragment).

CN JAG2.

OS Rattus norvegicus (Rat).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

[1]

SEQUENCE FROM N.A.

RP TISSUE:Brain;

RX MEDLINE=97105852; PubMed=8948600;

PA Shawber C., Boultter J., Lindseil C.E., Weinmaster G.;

RA "Jagged2: a serrate-like gene expressed during rat embryogenesis.";

RL Dev. Biol. 180:370-376 (1996).

CC FUNCTION: Putative Notch ligand involved in the mediation of Notch signaling. May have a role in neurogenesis in the peripheral nervous system, limb development and in the adult brain.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- DEVELOPMENTAL STAGE: At stage E12.5 it is detected in dorsal root ganglia, AER, and surface ectoderm. At E14.5, found as well in cranial ganglia, thymus and olfactory epithelia. At E16.5, found as well in salivary gland, tooth buds and hair follicles.

CC -!- SIMILARITY: Contains 16 EGF-like domains.

CC -!- SIMILARITY: Contains 1 DSL domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: U70050; AAC52946.1; -

DR HSSP; P00743; ICF2.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0008083; P:growth factor activity; ISS.

DR GO; GO:0005112; P:Notch binding; NAS.

DR GO; GO:0007605; P:hair cell cycle; ISS.

DR GO; GO:0007049; P:cell differentiation; NAS.

DR GO; GO:00020154; P:cell fate commitment; ISS.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0009912; P:cell migration; ISS.

DR GO; GO:0007605; P:hair cell fate commitment; ISS.

DR GO; GO:0003036; P:limb morphogenesis; NAS.

DR GO; GO:0003034; P:N signaling pathway; NAS.

DR GO; GO:0002129; P:regulation of cell proliferation; ISS.

DR GO; GO:0002127; P:regulation of cell proliferation; ISS.

DR GO; GO:0002017; P:cell differentiation; ISS.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0009912; P:cell migration; ISS.

DR GO; GO:0007605; P:hair cell fate commitment; ISS.

DR GO; GO:0003036; P:limb morphogenesis; NAS.

DR GO; GO:0003034; P:N signaling pathway; NAS.

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DR GO; GO:0002017; P:cell differentiation; ISS.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0009912; P:cell migration; ISS.

DR GO; GO:0007605; P:hair cell fate commitment; ISS.

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DR GO; GO:0003034; P:N signaling pathway; NAS.

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DR GO; GO:

FT	DOMAIN	586	622	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).	
FT	DOMAIN	623	656	EGF-LIKE 16.	
FT	DOMAIN	658	686	EGF-LIKE 17.	
FT	DOMAIN	688	724	EGF-LIKE 18.	
FT	DOMAIN	726	762	EGF-LIKE 19.	
FT	DOMAIN	764	800	EGF-LIKE 20.	
FT	DOMAIN	803	839	EGF-LIKE 21.	
FT	DOMAIN	841	877	EGF-LIKE 22.	
FT	DOMAIN	878	924	EGF-LIKE 23.	
FT	DOMAIN	926	962	EGF-LIKE 24.	
FT	DOMAIN	964	1000	EGF-LIKE 25.	
FT	DOMAIN	1002	1040	EGF-LIKE 26.	
FT	DOMAIN	1042	1081	EGF-LIKE 27.	
FT	DOMAIN	1083	1122	EGF-LIKE 28.	
FT	DOMAIN	1126	1167	EGF-LIKE 29.	
FT	REPEAT	1168	1208	LIN/NOTCH 1.	
FT	REPEAT	1209	1242	LIN/NOTCH 2.	
FT	REPEAT	1243	1282	LIN/NOTCH 3.	
Db	Query Match Best Local Similarity Matches 33; Conservative 8; Mismatches 48; Gaps 6;	Score 96; DB 1; Length 1964;	Pred. No. 0.13; Indels 34;		
Qy	15 ISACAMLLC-HGGSLQHTFQQFHHLRPGEGTCTPCKH--	-----EVIAAHR--CCNKNR	58		
Db	689 IGGCISTPCPAHGCTHP-----QPSGYNCTCPAGYMGITCEVETACHSGPCLNGGSC	741			
Qy	59 ERSQTIVKCSLCPGKVAGTTANRNPSCVDASIVIGRWCMPCEBECKKLPLDNGWMC	118			
Db	742 SIRPEGYSTCLP--SHTGRHCQTAVD-----HCVSSASLNGGTCVNKPGETFFCCLC	790			
Qy	119 ATG 121			"The Notch receptor is cleaved constitutively by a furin-like convertase.",	
Db	791 ATG 793			Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).	
RESULT 3					
NTC1_MOUSE	ID NTC1_MOUSE STANDARD; PRT; 2531 AA.				
AC Q01705; Q006007; Q61915; Q9QJC2; Q9QX7;					
DT 01-NOV-1995 (Rel. 32, Created)					
DT 01-FEB-1996 (Rel. 33, Last sequence update)					
DT 10-OCT-2003 (Rel. 42, Last annotation update)					
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A) (mT14) (p3300).					
GN NOTCH1 OR NOTCH					
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OC					
OX NCBI_TaxID=10090;					
RN [1]	SEQUENCE FROM N.A. (ISOFORM 1).				
RP TISSUE-Embryo;					
RC MEDLINE=93194170; PubMed=8449489;					
RA Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A., Copeland N.G., Gridley T.,					
RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";					
RT Genomics 15:259-264 (1993).					
RN [2]	SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.				
RP STRAIN=CD-1; TISSUE=Embryo;					
RC MEDLINE=93050801; PubMed=1426644;					
RA Reaume A.G., Conlon R.A., Zirngibl R., Yamaguchi T.P., Rossant J.; RT "Expression analysis of a Notch homologue in the mouse embryo.";					
RL Dev. Biol. 154:377-387(1992).					
RN [3]	SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.				
RP TISSUE=Embryo;					
RC MEDLINE=93058835; PubMed=1425352;					
RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M., Greenspan R.J., McMahon A.P., Gridley T.,					
RT "Expression pattern of Motch, a mouse homolog of Drosophila Notch,"					

suggests an important role in early postimplantation mouse development.";

RT Development 115:737-744 (1992).

RL RN [4]

RP SEQUENCE OF 1161-1547 FROM N.A.

RC STRAIN=CS7BL/6 X CBA; TISSUE=Embryo;

RA MEDLINE=93178563; PubMed=8440332;

RA Lardelli M., Lendahl U.;

RT "Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissues";

RT Exp. Cell Res. 204:364-372 (1993).

RL RN [5]

RP SEQUENCE OF 1659-1673 FROM N.A.

RA MEDLINE=93364499; PubMed=10437788;

RA Lee J.S., Ishimoto A., Yanagawa S.I.;

RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";

RT FEBS Lett. 455:276-280 (1999).

RL RN [6]

RP SEQUENCE OF 1950-2201 FROM N.A.

RA MEDLINE=9329496; PubMed=9384671;

RA Messerle M., Folio M., Nehls M., Eggerl H., Boehm T.;

RT "Dynamic changes in gene expression during in vitro differentiation of stem/embryonic stem cells";

RL Cytokines Cell. Mol. Ther. 1:139-143 (1995).

RL RN [7]

RP SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND

RP MUTAGENESIS OF 1651-ARG-ARG-1654.

RA MEDLINE=98318619; PubMed=9653148;

RA Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G., Israel A.;

RA "The Notch1 receptor is cleaved constitutively by a furin-like convertase";

RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).

RL RN [8]

RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.

RA MEDLINE=21523956; PubMed=11518718;

RA PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.

RA MEDLINE=21523950; PubMed=11226752;

RA "Murine notch homolog (N-1-4) undergo presenilin-dependent proteolysis";

RL J. Biol. Chem. 276:40268-40273 (2001).

RL RN [9]

RP POST-TRANSLATIONAL PROCESSING.

RA MEDLINE=21374376; PubMed=11451941;

RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

RT "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members";

RL Proc. Natl. Acad. Sci. U.S.A. 98:3026-3031 (2001).

RL RN [10]

RP INTERACTION WITH DTX2.

RA MEDLINE=211223750; PubMed=11226752;

RA Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S., Nakao K., Kinoshita T., Kadessh T., Hui C.-C., Artavanis-Tsakonas S., Okano H., Matsuno K.;

RT "Murine homologs of delta/ex define a novel gene family involved in vertebrate Notch signaling";

RL Int. J. Dev. Neurosci. 19:21-35 (2001).

CC JAGGED1, JAGGED2 and DELTA to regulate cell-fate determinants

CC Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with

CC RBP-J kappa and activates genes of the enhancer of split locus

CC Affects the implementation of differentiation, proliferation and

CC apoptotic programs (By similarity). May play an essential role in

CC postimplantation development, probably in some aspect of cell

CC specification and/or differentiation. May be involved in mesoderm

CC development, somite formation and neurogenesis. Involved in the

CC maturation of both CD4+ and CD8+ cells in the thymus.

CC SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-

CC terminal fragment N(BC) which are probably linked by disulfide

CC bonds. Interacts with DTX1 and DTX2.

CC SUBCELLULAR LOCATION: Type I membrane protein. Following

CC proteolytical processing NICD is translocated to the nucleus.

-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=";
IsoID=Q01705_1; Sequence=Displayed;

CC Name=2;
IsoID=Q01705_2; Sequence=VSP_001402, VSP_001403, VSP_001404;
Note=No experimental confirmation available;
TISSUE_SPECIFICITY: Highly expressed in the brain, lung and thymus. Expressed at lower levels in the spleen, bone marrow, spinal cord, eyes, mammary gland, liver, intestine, skeletal muscle, kidney and heart.

CC DEVELOPMENTAL_STAGE: First detected in the mesoderm at 7.5 dpc. By 8.5 dpc highly expressed in presomitic mesoderm, mesenchyme and endothelial cells, while much lower levels are seen in the neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in the neuroepithelium. At 13.5 dpc expressed in the surface ectoderm, eye and developing whisker follicles.

CC PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.

CC PTM: Phosphorylated.

CC SIMILARITY: Belongs to the NOTCH family.
CC SIMILARITY: Contains 36 EGF-like domains.
CC SIMILARITY: Contains 3 Lin-Notch repeats.
CC SIMILARITY: Contains 5 ANK repeats.

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CC MGD; MGI:97363; Notch1.
DR GO; GO:0005887; C:integral to plasma membrane; IC.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0030154; P:cell differentiation; IMP.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007219; P:N signaling pathway; IC.
DR GO; GO:045944; P:positive regulation of transcription from P. . ; IDA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyL_S.
DR InterPro; IPR001681; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR002110; Laminin_EGF.
DR InterPro; IPR008297; Notch_Notch_dom.
DR Pfam; PF00023; ank; 7.
DR Pfam; PF00008; EGF_35.
DR Pfam; PF00666; notch_3.
DR Pfam; PF00227; Notch_1.
DR Prints; PR00010; EGFBLOOD.
DR Prints; PR00011; EGFLAMININ.
DR Prints; PR01452; NOTCH.

CC SMART; SM00248; ANK; 6.
SMART; SM00119; EGF_Ca; 24.
SMART; SM00094; NL_2.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS50026; EGF_3; 36.
KW Receptor; transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation; Alternative splicing.
KW POTENTIAL.
FT SIGNAL 1 18
FT CHAIN 19 2531
FT CHAIN 1711 2531
FT CHAIN 1744 2531
FT DOMAIN 19 1725
Query Match 12.7%; Score 95.5; DB 1; Length 2531;
Best Local Similarity 26.8%; Pred. No. 0.2;
Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;
Cys 15 ISACAMLICSLQHHTQQHHLRPGGTCB-VIAHRC-----CNGN 56
Db 679 IDECAGSPCH----NGCTEDGFDAGFTCPCEGYHDPTCLSEVNENCSN 723
From 57 ----REERSQTWVKSCLPGKVAGTRNRFSPCVDAIVIGKWWCEMPCELEGGCKTLP 111
Db 724 PCIHGARDGLNGYKCDAPS-WSGTNCD-----INNNNECESNPVCYNGGTCKDM- 771
Oy 112 DNSGMNC 118
Db 772 -TSGYVC 777

RESULT 4
NTC1_RAT STANDARD; PRT; 2531 AA.
ID NTC1_RAT
AC Q07056;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1).
GN NOTCH.
Ox Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N_A.
RN TISSUE-Schwann cell;
RX MEDLINE=92111383; PubMed=1764995;
RA Weinmaster G.; Roberts V.J.; Lemke G.;
RA "A homolog of Drosophila Notch expressed during mammalian development";
RT Development 113:199-205 (1991).
RL REVISTONS TO 1652-1653.
RA Weinmaster G.;
RA Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
[2]
RN FUNCTION.
RX MEDLINE=21094508; PubMed=11182080;
RA Tanigaki K.; Nogaki F.; Takahashi J.; Tashiro K.; Kurooka H.;
RA Honjo T.;
RA "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent neural progenitor cells to an astroglial fate";
RL Neuron 29:45-55(2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=93202015; PubMed=1295745;

RA	Weinmaster G., Roberts V.J., Lemke G.; "Notch2: a second mammalian Notch gene." [5]	DR	PIRSF002279; Notch; 1.
RT	Development 116:931-941(1992).	DR	PRINTS; PRO0011; EGFBLOOD.
RL		DR	PRINTS; PRO0010; EGFBLOOD.
RN		DR	PRINTS; PRO1452; NOTCH.
RP	TISSUE SPECIFICITY	DR	SMART; SM00248; ANK; 6.
RX	MEDLINE=2131789; PubMed=11438922;	DR	SMART; SM00179; EGF CA; 25.
RA	Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.; "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-NSL signaling system during brain development." [6]	DR	PROSITE; PS00297; ANK REP REGION; 1.
RT	J. Comp. Neurol. 436:167-181(2001).	DR	PROSITE; PS00088; ASX HYDROXYL; 22.
RL	Jagged1, Jagged2 and Delta1 as a receptor for membrane-bound ligands upon ligand activation through the released notch intracellular domain (NICD), it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). Acts instructively to control the cell fate determination of CNS multipotent progenitor cells, resulting in astrogliial induction and neuron/oligodendrocyte suppression.	DR	PROSITE; PS00010; ASX HYDROXYL; 4.
CC	-	DR	PROSITE; PS00022; EGF_1; 15.
CC	Jagged1, Jagged2 and Delta1 as a receptor for membrane-bound ligands upon ligand activation through the released notch intracellular domain (NICD), it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). Acts instructively to control the cell fate determination of CNS multipotent progenitor cells, resulting in astrogliial induction and neuron/oligodendrocyte suppression.	DR	PROSITE; PS00026; EGF_2; 26.
CC	-	DR	PROSITE; PS01187; EGF_3; 36.
CC	-	DR	PROSITE; PS01187; EGF CA; 21.
CC	-	DR	KW Receptor; Transcription Protein; Repetitve; ANK repeat; EGF-like domain; KW Developmental Protein; Repeat; ANK repeat; EGF-like domain; KW Transmembrane; Glycoprotein; Signal; Phosphorylation.
CC	-	FT	POTENTIAL.
CC	-	FT	NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
CC	-	FT	NOTCH EXTRACELLULAR TRUNCATION (BY SIMILARITY).
CC	-	FT	NOTCH INTRACELLULAR DOMAIN (BY SIMILARITY).
CC	-	FT	EXTRACELLULAR (POTENTIAL).
CC	-	FT	POTENTIAL.
CC	-	FT	CYTOSPLASMIC (POTENTIAL).
CC	-	FT	EGF-LIKE 1.
CC	-	FT	EGF-LIKE 2.
CC	-	FT	EGF-LIKE 3.
CC	-	FT	EGF-LIKE 4.
CC	-	FT	EGF-LIKE 5.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 6.
CC	-	FT	EGF-LIKE 7.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 8.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 9.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 10.
CC	-	FT	EGF-LIKE 11.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 12.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 13.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 14.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 15.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 16.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 17.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 18.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 19.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 20.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 21.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 22.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 23.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 24.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 25.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 26.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 27.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 28.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 29.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 30.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 31.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	FT	EGF-LIKE 32.
CC	-	FT	CALCIUM-BINDING (POTENTIAL).
CC	-	EMBL; X57405; CAA00667; 1/-.	LIN/NOTCH 1.
CC	-	DR	HSSP; P00740; 1EDM.
CC	-	DR	InterPro; IPR002110; ANK.
CC	-	DR	InterPro; IPR000152; Asx hydroxy1_S.
CC	-	DR	InterPro; IPR000742; EGF_2.
CC	-	DR	InterPro; IPR01188; EGF_Ca.
CC	-	DR	InterPro; IPR001438; EGF_II.
CC	-	DR	InterPro; IPR006209; EGF_Like.
CC	-	DR	InterPro; IPR00049; Laminin_EGF.
CC	-	DR	InterPro; IPR008297; Notch.
CC	-	DR	InterPro; IPR00080; Notch_dom.
CC	-	DR	Pfam; PF00023; ank; 6.
CC	-	DR	Pfam; PF00008; EGF; 35.
CC	-	DR	Pfam; PF00066; notch; 3.

FT	DOMAIN SITE	2497 1654	2500 1655	POLY-SER. CLEAVAGE BY (FURIN-LIKE PROTEASE) (BY SIMILARITY.
FT	DISULFID	24	37	BY SIMILARITY.
FT	DISULFID	31	46	BY SIMILARITY.
FT	DISULFID	48	57	BY SIMILARITY.
FT	DISULFID	63	74	BY SIMILARITY.
FT	DISULFID	68	87	BY SIMILARITY.
FT	DISULFID	89	98	BY SIMILARITY.
FT	DISULFID	106	117	BY SIMILARITY.
FT	DISULFID	111	127	BY SIMILARITY.
FT	DISULFID	129	138	BY SIMILARITY.
FT	DISULFID	144	155	BY SIMILARITY.
FT	DISULFID	149	164	BY SIMILARITY.
FT	DISULFID	166	175	BY SIMILARITY.
FT	DISULFID	182	195	BY SIMILARITY.
FT	DISULFID	189	204	BY SIMILARITY.
FT	DISULFID	206	215	BY SIMILARITY.
FT	DISULFID	222	233	BY SIMILARITY.
FT	DISULFID	227	243	BY SIMILARITY.
Query Match Score	12.7%	Score 95.5;	DB 1;	Length 2531;
Best Local Similarity	26.8%	Pred. No. 0, 2;	;	
Matches	34;	Conservative	7;	Mismatches 35;
Qy	15	ISACAMILCHGSLOHTFQOHHLHRPEGGTCE-VIAAHRC-	-CNKN 56	
Db	679	IDECAGSICH-----NGTCTEDGIAAGTCRCPGYHADPTCLSEVNNECSNSN	723	
Qy	57	--RIBERSQTQVKCSCSLPQKGVAGTTRNRPSCVDASIVIGKWCMEPCLGRECKTLP	111	
Db	724	PCIHGACRDGLNGYKCDAPG-WSGTNCD-----INNNCEESNPVCNGGTCKDM-	771	
Qy	112	DNSGWMC 11 8		
Db	772	-TSGYVC 777		
RESULT	5			
CRB_DROME	ID	CRB_DRDOME	STANDARD;	PRT; 2139 AA.
AC	P10640;	01-MAR-1989 (Rel. 10, Created)		
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Crumbs protein precursor (95F).			
GN	Drosophila melanogaster (Fruit Fly).			
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydriodea; Drosophilidae; Drosophila.			
OX	NCBI_TAXID=7227;			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=Oregon-R; TISSUE=Embryo;			
RX	MEDLINE=90263104; Pubmed=244615;			
RA	"Crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila epithelial cells and required for organization of epithelia.";			
RT	Cell 61:787-799(1990).			
RN	SEQUENCE OF 1663-1955 FROM N.A.			
RC	TISSUE=Embryo;			
RX	MEDLINE=8721537; PubMed=3107986;			
RA	Knust E., Dietrich U., Tepas U., Bremer K.A., Weigel D., Vaessin H., Campos-Ortega J.A.,			
RA	"EGF homologous sequences encoded in the genome of Drosophila melanogaster, and their relation to neurogenic genes";			
RT	EMBO J. 6:761-766(1987).			
RL	FUNCTION: May play a role in the development of epithelia, possibly for the establishment and/or maintenance of cell polarity. It may act as a signal.			
CC				
CC				

CC !- SUBCELLULAR LOCATION: Type I membrane protein. CC !- PTM: PHOSPHORYLATED IN THE CYTOPLASMIC DOMAIN (POTENTIAL). CC !- SIMILARITY: Contains 3 laminin G-like domains.

CC !- SIMILARITY: Contains through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC !- ALT_SEQ.: AAA2B28.1; EMBL: M33753; PIR: A35144; CRN28793.1; DR PIR: A35672; A35672.

CC !- ESTABLISHMENT AND/OR MAINTENANCE OF CELL PO. : ; IMP. P:establishment and/or maintenance of polarit. : ; IMP. P:establishment and/or maintenance of polarit. : ; IMP.

CC !- C:APICAL PLASMA MEMBRANE; IDA; C:ACICOLATERAL PLASMA MEMBRANE; IDA; GO; GO:0016324; C:zonula adherens assembly; IMP. GO; GO:0016327; C:zonula adherens maintenance; IMP. GO; GO:0007163; P:establishment and/or maintenance of cell po. : ; IMP. GO; GO:0016332; P:establishment and/or maintenance of polarit. : ; IMP. GO; GO:0045334; P:photoreceptor maintenance; IMP. GO; GO:0042052; P:rhabdomere development; NAS.

CC !- C:APICAL PLASMA MEMBRANE; IDA; DR InterPro: IPR000985; ConA-like_lec_gly. DR InterPro: IPR000742; EGF_7.

CC !- C:APICAL PLASMA MEMBRANE; IDA; DR InterPro: IPR001438; EGF_T1. DR InterPro: IPR006209; EGF_Like. DR InterPro: IPR00049; Laminin_EGF.

CC !- C:APICAL PLASMA MEMBRANE; IDA; DR InterPro: IPR001791; Laminin_G. Pfam: PF00008; EGF; 26. Pfam: PF00054; Laminin_G; 3.

CC !- PRINTS; PR00010; EGF_EGFLDD. DR SMART; SM00179; EGF CA; 11. DR SMART; SM00282; LamG; 3.

CC !- ASX_HYDROXYL; 15. DR PROSITE; PS00010; ASX_HYDROXYL. DR PROSITE; PS00022; EGF 1; 26. DR PROSITE; PS50066; EGF 2; 17. DR PROSITE; PS00187; EGF 3; 27. DR PROSITE; PS50025; LAM_G_DOMAIN; 3. DR Differentiation; Repeat_EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation. KW SIGNAL 1 90 CRUMBS PROTEIN. FT DOMAIN 91 2139 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 2085 2084 POTENTIAL.

FT DOMAIN 2112 2111 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 267 2139 EGF-LIKE 1.

FT DOMAIN 303 303 EGF-LIKE 2.

FT DOMAIN 348 386 EGF-LIKE 3.

FT DOMAIN 388 425 EGF-LIKE 4.

FT DOMAIN 427 463 EGF-LIKE 5.

FT DOMAIN 464 500 EGF-LIKE 6.

FT DOMAIN 501 532 EGF-LIKE 7.

FT DOMAIN 545 581 EGF-LIKE 8.

FT DOMAIN 582 611 EGF-LIKE 9.

FT DOMAIN 609 646 CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 648 685 EGF-LIKE 11.

FT DOMAIN 687 723 CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 725 761 EGF-LIKE 13.

FT DOMAIN 763 800 EGF-LIKE 14.

FT DOMAIN 802 838 EGF-LIKE 15.

FT DOMAIN 840 902 EGF-LIKE 16.

FT DOMAIN 904 940 EGF-LIKE 17.

FT DOMAIN 942 978 EGF-LIKE 18.

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- CC STRAIN=Berkeley; PubMed=20196016; ID NOTC_DROME; STANDARD; PRT; 2703 AA.
 CC ADAMS M.D., Celinkin S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Gocayne J.D., White O., Adams M.D., Kerlavage A.R., Ballew R.F.,
 CC Givan S.L., Glavina D.T., Utley A.M., Zaranowski S., Hoadson S.N.,
 CC Amanatides P.G., Scheer S.E., Richards S., Ashburner M., Henderson S.N.,
 CC George R.A., Lewis S.E., Richards S., DBD0001389; ctdD.
 DR Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 DR Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D.,
 DR Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G.,
 DR Baldwin D., Agbayani A., Bayraktaroglu C., Beasley E.M.,
 DR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchvarov S.,
 DR Ballev R.M., Basu A., Baxendale J., Bouck J., Boisclair E., Brottier P.,
 DR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchvarov S.,
 DR Borkova D., Botchvarov M.R., Bouck J., Brodin D.A., Butler H., Cadieu E., Center A., Chandra I.,
 DR Abrial J.F., Agbayani A., Bayraktaroglu C., Beasley E.M.,
 DR Ballev R.M., Basu A., Baxendale J., Bouck J., Boisclair E., Brottier P.,
 DR Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Botchvarov S.,
 DR Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 DR Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P.,
 DR de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I.J., Dietz S.M.,
 DR Dodson K., Douc L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 DR Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 DR Fosler C., Gabrielian A.E., Garg N.S.S., Gelbart W.M., Glasser K.,
 DR Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 DR Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 DR Hostin D., Houston K.A., Howell T.J., Wei M.-H., Ibegwam C.,
 DR Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 DR Kimmel B.E., Kodira C.D., Kraft S., Kravitz S., Kulp D., Lai Z.,
 DR Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 DR Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 DR Merkulov G., Millashka N.Y., Mobarry C., Morris J., Mosherf A.,
 DR Mount S.M., Moy M., Murphy L., Murray D.M., Nelson D.L.,
 DR Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclob J.M.,
 DR Palazzolo M., Pittman G.S., Saunders R.D.C., Scheeler F., Shen H.,
 DR Reineke K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 DR Shue B.C., Sider-Kianos I., Simpson M., Skupski M.P., Smith T.,
 DR Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 DR Svistres R., Tector C., Turner R., Wenter E., Wang A.H., Wang X.,
 DR Wang Z.-Y., Wasserman D.A., Weissenbach J.,
 DR Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.-A.,
 DR Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 DR Zheng X.-H., Zhong F.-N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 DR Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 DR "The genome segment of *Drosophila melanogaster*,"
 DR Science 287:2185-2195 (2000).
 DR [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Oregon R;
 RC MEDLINE=20196011; ID NOTC_DROME; PRT; 2703 AA.
 RX SEQUENCE OF 2505-2611 FROM N.A.
 RA Benos P.V., Gatt M.K., Ashburner M., Harris D., Murphy L., Murphy D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demaile J., Cadieu E.,
 RA Dreano S., Gloux S., Leilaire V., Moctier S., Galibert F., Borkova D.,
 RA Minana B., Kafatos F.C., Louis C., Siden-Kianos I., Bolshakov S.,
 RA Papagannakis G., Spanos I., Cox S., Madueno B., de Pablo B.,
 RA Modolell J., Peter A., Schoettler P., Werner M., Mourklis P.,
 RA Beinert N., Dowe G., Schaeffer U., Jaekle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamtisou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of *D. melanogaster*,"
 RT Science 287:2220-2222 (2000).
 RN [5]
 RN SEQUENCE OF 1-8 FROM N.A.
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE=85099322; ID NOTC_DROME; PRT; 2703 AA.
 RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
 RT "op: a novel family of transcribed repeats shared by the Notch locus
 RT and other developmentally regulated loci in *D. melanogaster*,"
 RT Cell 40:55-62 (1985).
 RN [6]
 RN SEQUENCE OF 1-8 FROM N.A.
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE=87257846; ID NOTC_DROME; PRT; 2703 AA.
 RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
 RT "Sequence of the notch locus of *Drosophila melanogaster*: relationship
 RT of the encoded protein to mammalian clotting and growth factors.";
 RL Mol. Cell. Biol. 6:3094-3108 (1986).
 RN [7]
 RP INTERACTION WITH DX, AND MUTANT SU42C.

- :- SIMILARITY: Contains 6 ANK repeats.

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CC -----

DR EMBL; M16152; AAA859220.1; -.
 DR EMBL; M16153; AAA859220.1; JOINED.
 DR EMBL; M16159; AAA859220.1; JOINED.
 DR EMBL; M16150; AAA859220.1; JOINED.
 DR EMBL; M16151; AAA859220.1; JOINED.
 DR EMBL; K03508; AAA28725.1; -.
 DR EMBL; K03509; AAA28725.1; JOINED.
 DR EMBL; K03510; AAA28725.1; JOINED.
 DR EMBL; K03511; AAA28725.1; JOINED.
 DR EMBL; AB003426; AAF45448.2; -.
 DR EMBL; AL035436; CAB37610.1; -.
 DR EMBL; AL035439; CAB37610.1; JOINED.
 DR EMBL; ML2175; AAA74496.1; -.
 DR EMBL; M16025; AAA28726.1; -.

Query Match Score 86.5; DB 1; Length 2703;
 Best Local Similarity 25.9%; Pred. No. 1.7;
 Matches 22; Conservative 10; Mismatches 34; Indexes 19; Gaps 3;

QY 40 EGGSCTEV---IAAHRCCKNKRIEERSQTVKCSCLPGKVA-----GTTTNRPS 83
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 12124 QGQNCEINTDDCAPNPCONGGTCHDYRMNFSCPPGTMGICEINRDKPQGACHNGS 1.273
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 QY 84 CVDASITVIGKWCMEEMPELEGHECK 108
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 1274 CIDR--VGGFEFCVQQGFGVGRCE 1295
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 RESULT 9

DLL4_HUMAN STANDARD; PRT; 685 AA.
 AC Q9NQ71; Q9NQ79.
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Delta-like protein 4 precursor (Drosophila Delta homolog 4)
 DE (UNQ1895/PRO4341).
 GN DLL4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX [1] _TaxID=9606;
 RN SEQUENCE FROM N.A.
 RP TISSUE=brain;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Yoneya T., Tahara T., Nagao K., Yamada Y., Yamamoto T., Miyakuni S.,
 RA Niishikawa M.,
 RA "Molecular cloning of Delta-4, a new mouse and human Notch ligand.";
 RT Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=22887296; PubMed=12875319;
 RA Clark H. F., Grunberg A. I., Baker K., Baldwin D., Brush J.,
 RA Abaya E.,
 RA "Molecular cloning of Delta-4, a new mouse and human Notch ligand.";

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Hwang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wiegand D., Woods K., Xie M.-H., Yanbura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goodard A., Wood W.I., Godowski P.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment"; *Biochem Res. Lett.* 13:2265-2270 (2003). [5]

SEQUENCE OF 33-685 FROM N.A.
RC TISSUE=Placenta;
RA Mailhos C., Modlich U., Harris J., Lewis J., Bicknell R., RA Ish-Horowicz D.; "A novel Delta gene expressed in embryonic and tumour vasculature.";
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL -!
CC -!- FUNCTION: Plays a role in the Notch signaling pathway. Activates
CC Notch-1 and Notch-4 (By similarity).
CC -!- SUBUNIT: Binds to Notch-1 and Notch-4 (By Similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in vascular endothelium.
CC -!- DOMAIN: The Delta-Serrata-Lag2 (DSL) domain is required for
CC binding to the Notch receptor.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.

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DR AF253468; NAP76427_1; -;
EMBL; AB036331; BAB16085_1; -;
DR AB04894; BAB16881_1; -;
EMBL; AY358894; AAQ89253_1; -;
DR AF279405; AAP1912_1; -;
DR PIR:JC7570; JC7570.
DR HSSP; P00740; 1EDM.
Genew; HGNC:2910; DLL4.
MIM; 605215; -;
DR GO; GO:0005112; F:Notch binding; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:007165; P:signal transduction; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_Like.
DR Pfam; PF01144; DSL_1.
DR Pfam; PF00008; EGF_7.
DR PRINTS; PRO0010; EGFBLOOD.
DR SMART; SM00051; DSL_1.
DR PROSITE; PS00010; ASX_HYDROXYL_1.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
KW Signal; EGF-Like domain; Repeat; Transmembrane; Developmental protein; Differentiation; Glycoprotein.
FT SIGNAL_1; POTENTIAL.
FT CHAIN_27; EXTRACELLULAR_PROTEIN_4.
FT DOMAIN_27; EXTRACELLULAR (POTENTIAL).
FT TRANSMEM_530; POTENTIAL.
FT DOMAIN_551; CYTOPLASMIC (POTENTIAL).

FT DOMAIN_155; DSL.
FT DOMAIN_217; EGF-LIKE_1.
FT DOMAIN_251; EGF-LIKE_2.
FT DOMAIN_282; EGF-LIKE_3.
FT DOMAIN_322; EGF-LIKE_4.
FT DOMAIN_360; EGF-LIKE_5.
FT DOMAIN_400; EGF-LIKE_6.
FT DOMAIN_438; EGF-LIKE_7.
FT DOMAIN_440; EGF-LIKE_8.
FT DOMAIN_480; EGF-LIKE_9.
FT DISULFID_218; BY SIMILARITY.
FT DISULFID_252; BY SIMILARITY.
FT DISULFID_284; BY SIMILARITY.
FT DISULFID_324; BY SIMILARITY.
FT DISULFID_362; BY SIMILARITY.
FT DISULFID_402; BY SIMILARITY.
FT DISULFID_438; BY SIMILARITY.
FT DISULFID_440; BY SIMILARITY.
FT DISULFID_480; BY SIMILARITY.
FT DISULFID_518; BY SIMILARITY.
FT DISULFID_222; BY SIMILARITY.
FT DISULFID_226; BY SIMILARITY.
FT DISULFID_241; BY SIMILARITY.
FT DISULFID_250; BY SIMILARITY.
FT DISULFID_253; BY SIMILARITY.
FT DISULFID_259; BY SIMILARITY.
FT DISULFID_270; BY SIMILARITY.
FT DISULFID_272; BY SIMILARITY.
FT DISULFID_288; BY SIMILARITY.
FT DISULFID_294; BY SIMILARITY.
FT DISULFID_310; BY SIMILARITY.
FT DISULFID_312; BY SIMILARITY.
FT DISULFID_321; BY SIMILARITY.
FT DISULFID_328; BY SIMILARITY.
FT DISULFID_339; BY SIMILARITY.
FT DISULFID_348; BY SIMILARITY.
FT DISULFID_350; BY SIMILARITY.
FT DISULFID_359; BY SIMILARITY.
FT DISULFID_366; BY SIMILARITY.
FT DISULFID_371; BY SIMILARITY.
FT DISULFID_390; BY SIMILARITY.
FT DISULFID_399; BY SIMILARITY.
FT DISULFID_406; BY SIMILARITY.
FT DISULFID_411; BY SIMILARITY.
FT DISULFID_426; BY SIMILARITY.
FT DISULFID_428; BY SIMILARITY.
FT DISULFID_437; BY SIMILARITY.
FT DISULFID_444; BY SIMILARITY.
FT DISULFID_466; BY SIMILARITY.
FT DISULFID_475; BY SIMILARITY.
FT DISULFID_484; BY SIMILARITY.
FT DISULFID_495; BY SIMILARITY.
FT DISULFID_495; BY SIMILARITY.
FT CARBOYD_108; N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOYD_183; N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOYD_183; N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOYD_205; N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOYD_393; N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE_685_AA; 74604 MW; 6CF89D3C220AAC89 CRC64;

Query Match 11.4%; Score 86; DB: 1; Length 685;
Best Local Similarity 25.0%; Pred. No. 0.45; Mismatches 9; Indels 30; Gaps 6;
Matches 28; Conservative 14. WISAC---AMILCHGSLOHTFOQHHLHRPREGTCEVIAHRCNKNRIBERSQTVKCSC 69
Oy DB 268 WQCTCDEGWGGIFCDDLNTC-TTHSPCKNGATC-----SNSGSRSYT-CRC 312
Oy 70 LPGKVAGTTNRPSVCDASIVGRWCMEPCLEGECCKTLPDNSGWMCATG 121
Oy 313 RPYTG-----VDCELELSE--CDSNPCRNGGSKDQEDGYHCLCPG 353
RESULT 10
JAG1_HUMAN
ID JAG1_HUMAN STANDARD PRT; 1218 AA.
AC P78504; O14902; O15816;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Jagged_1 precursor (Jagged1) (hJ1).
GN JAG1 OR JAGL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteridae; Primates; Catarrhini; Hominoidea; Homo.
RN [1] NCBI_TaxID=9606;
RN [1] _TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=97422615; PubMed=9268641;
RX Oda T.; Elkahloun A.G.; Melitter P.S.; Chandrasekharappa S.C.;
RX "Identification and cloning of the human homolog (JAG1) of the rat Jagged gene from the Alagille syndrome critical region at 20p12.";
RX Genomics 43:376-379(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT AGS CYS-184.

- L** TISSUE=Bone marrow; PubMed=9207788;
 RX MEDLINE=97351506; PubMed=9207787;
 RA Oda T., Elkhalou A.G., Pike B.I., Okajima K., Krantz I.D., Genin A.,
 RA Piccoli D.A., Meltzer P.S., Spinner N.B., Collins F.S.,
 RA Chandrasekharappa S.C.;
 RA "Mutations in the human Jagged1 gene are responsible for Alagille
 syndrome." ;
 RT Nat. Genet. 16:235-242 (1997).
 RL [9]
 RN RN
 RP RP
 SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=9812342; PubMed=9462510;
 RA Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L.,
 RA Marcovali S., Friedman C., Trask B.J., Hood L., Torok-Storb B.,
 RA "The human homolog of rat Jagged1 expressed by marrow stroma inhibits
 RT differentiation of 32D cells through interaction with Notch1." ;
 RT Immunity 8:43-55 (1998).
 RL [4]
 RN RN
 SEQUENCE FROM N.A.
 RX MEDLINE=9262417; PubMed=10329626;
 RA Bash J., Zong W.-X., Banga S., Rivera A., Ballard D.W., Ron Y.,
 RA Gelinas C.;
 RT "Rel/NF kappaB can trigger the Notch signaling pathway by inducing the
 expression of Jagged1, a ligand for Notch receptors." ;
 RL [5]
 RN RN
 SEQUENCE FROM N.A.
 RX MEDLINE=919180765; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RT "Human ligands of the Notch receptor." ;
 RL Am. J. Pathol. 154:785-794 (1999).
 RN [6]
 RN RN
 SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA DeLousas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakley S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrell W.D., Butler A.P., Carder C., Carter S.Y., Clark S.Y.,
 RA Chapman J.C., Clamp M., Clark G., Connor R.E., Corby N.R.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deachman R.T., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Knights A., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehvastola M., Leversha S.L., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnaughey L.J., McIay K., McMurray A.A.,
 RA Milne S.A., Mistrey D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.J.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.L., Soderlin C., Stewart C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitemead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.;
 RT "The DNA sequence and comparative analysis of human chromosome 20." ;
 RL Nature 414:865-871 (2001).
 RN [7]
 RP RP
 SEQUENCE OF 14-1227 FROM N.A.
 RC TISSUE=Umbilical vein endothelial cells
 RX MEDLINE=97115768; PubMed=8955070;
 RA Macia G.T., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,
 RA Rogers J.;
 RT "An antisense oligonucleotide to the notch ligand jagged1 enhances
 RT fibroblast growth factor-induced angiogenesis in vitro." ;
 RL J. Biol. Chem. 271:32499-32502 (1996).
 RN [8]
 RP RP
 DISEASE.

CC decisions during hematopoiesis. Seems to be involved in early CC and late stages of mammalian cardiovascular development. Inhibits CC myoblast differentiation (in vitro). Enhances fibroblast growth factor-induced angiogenesis (in vitro).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.

CC In cervix epithelium expressed in undifferentiated subcolumnar reserve cells and squamous metaplasia. Expression is upregulated in cervical squamous cell carcinoma. Expressed in bone marrow cell-line HS-274 which supports the long-term maintenance of immature progenitor cells.

CC -!- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal cardiac outflow tract and pulmonary artery, major arteries, portal vein, optic vesicle, oocyst, branchial arches, metanephros, pancreas, mesocardium, around the major bronchial branches, and in the neural tube.

CC -!- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS) (MIM:118450). AGS is an autosomal dominant development disorder that affects structures in the liver, heart, skeleton, eye, kidney and other organs.

CC -!- DISEASE: Defects in JAG1 are a cause of tetralogy of Fallot (TOF) (MIM:187500). TOF is a congenital heart anomaly which consists of pulmonary stenosis, ventricular septal defect, dextroposition of the aorta (aorta is on the right side instead of the left), and hypertrophy of the right ventricle. This condition results in a blue baby at birth due to inadequate oxygenation.

CC Surgical correction is emergent.

CC -!- SIMILARITY: Contains 15 EGF-like domains.

CC -!- SIMILARITY: Contains 1 DSU domain.

CC -!- CAUTION: Ref. 7 sequence differs from that shown due to a frameshift in position 1187.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between Local Similarity 23.8%; Pred. No. 0.81; Matches 34; Conservative 11; Mismatches 34; Indels 64; Gaps 9;

Query Match 37 HPR-EFGCE-----VIAAHRC-----C-NKRNRIERQTVKCS 69
Best Local Similarity 23.8%; Pred. No. 0.81;
Matches 34; Conservative 11; Mismatches 34; Indels 64; Gaps 9;

Db 303 HQQLPLGNCNTNGPDKYQSCPPGSGPNCETABHACLSDPHNRGCKTSLGFBC 362

Query Match 70 LPGRKVAGTTRN-----PSCVDASTIVG-----KWW-----CEMEP 100
Db 363 SPEGWGPCTSTNTIDDCSPINCSHGGTCQD----LYNGFKCVCPPMTGKTCQLDANECAKP 420

Query Match 101 CLEGECKTLPDN-----SGWM 117
Db 421 CYNAKSCKNLIASYCDCLPGNM 443

RESULT 11
JAG1_MOUSE STANDARD; PRT; 1218 AA.
ID JAG1_MOUSE
AC Q9QXX0;
DT 28-FEB-2003 (Rel. 41, Created)
DI 15-MAR-2004 (Rel. 43, Last annotation update)
DE Jagged 1 precursor (Jagged1).
GN JAG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _SEQUENCE FROM N.A.; AND RECEPTOR INTERACTION.
RP SEQUENCE=Swiss Webster / NIH;
RC STRAIN=Swiss Webster / NIH;
RX MEDLINE=20020271; PubMed=10551863;
RA Shirizuka K., Kumano K., Hosoya N., Takahashi T., Kanda Y., Hamada Y., Yuzaki Y., Hiraki H.;
RT "Mouse Jagged1 physically interacts with Notch2 and other Notch receptors: assessment by quantitative methods.";
RT

J. Biol. Chem. 274:32961-32969 (1999).
[2] SEQUENCE FROM N.A.
RN RP STRAIN=C57BL/6; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shearer C.M., Schuler G.D., Altzschuler S.F., Zeeberg B.H., Bustow R.H., Max S.I., Wang J., Hsieh P., Hopkins R.P., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquaiello N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN TISSUE SPECIFICITY.
RX MEDLINE=20025757; PubMed=10556292;
RA Loomes K.M., Underkoffler L.A., Morabito J., Gottlieb S., Piccoli D.A., Spinner N.B., Baldwin H.S., Oakey R.J.; RT "The expression of Jagged1 in the developing mammalian heart correlates with cardiovascular disease in Alagille syndrome.";
RL Hum. Mol. Genet. 8:2443-2449 (1999).
RN FUNCTION: Ligand for multiple Notch receptors and involved in the mediation of Notch signaling. May be involved in cell-fate decisions during hematopoiesis. Seems to be involved in early and late stages of mammalian cardiovascular development. Inhibits myoblast differentiation (By similarity). May regulate fibroblast growth factor-induced angiogenesis.
CC -!- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed in many tissues, with highest expression in brain, heart, muscle and thymus.
CC -!- DEVELOPMENTAL STAGE: At 8.75-9.75 dpc expression was detected in structures that include those destined to contribute to the cardiovascular system of the adult heart. Expression was also detected in the mesencephalon and rhombencephalon.
CC -!- DOMAIN: The DSL domain is indispensable and sufficient for binding to NOTCH2.
CC -!- SIMILARITY: Contains 15 EGF-like domains.
CC -!- SIMILARITY: Contains 1 DSL domain.

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CC EMBL; APF15505_1; -;
DR EMBL; BC058675; AAH58675_1; -;
DR HSSP; P00740; IPDM;
DR MGD; MGI:105416; Jag1.
CC DR GO; GO:0005516; C:extracellular; ISS.
CC DR GO; GO:0005509; F:calcium ion binding; NAS.
CC DR GO; GO:0008083; F:growth factor activity; ISS.
CC DR GO; GO:0005312; F:Notch binding; IPD.
CC DR GO; GO:0005198; F:structural molecule activity; ISS.
CC DR GO; GO:0001525; F:angiogenesis; ISS.
CC DR GO; GO:0001079; F:cell fate determination; ISS.
CC DR GO; GO:0045446; F:endothelial cell differentiation; ISS.
CC DR GO; GO:030097; F:hemopoiesis; ISS.

-!- DEVELOPMENTAL STAGE: Expression is seen in E11.5-E14.5 embryos in four distinct regions of the ventricular zone in the developing spinal cord. Contains 15 EGF-like domains.

-!- SIMILARITY: Contains 1 DSU domain.

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DR EMBL; L38493; RABO6569.1; -.

DR HSSP; P00740; 1EDM.

DR GO; GO:0005576; C:extracellular; ISS.

DR GO; GO:0005887; C:integral to plasma membrane; ISS.

DR GO; GO:0008083; F:growth factor activity; ISS.

DR GO; GO:0005112; F:Notch binding; ISS.

DR GO; GO:0005198; F:structural molecule activity; ISS.

DR GO; GO:0001525; P:angiogenesis; ISS.

DR GO; GO:0001709; P:cell fate determination; NAS.

DR GO; GO:0045446; P:endothelial cell differentiation; ISS.

DR GO; GO:0030097; P:hemoapoiesis; ISS.

DR GO; GO:0030216; P:keratinocyte differentiation; ISS.

DR GO; GO:0044445; P:myoblast differentiation; ISS.

DR GO; GO:0007219; P:N signaling pathway; ISS.

DR GO; GO:0007399; P:neurogenesis; ISS.

DR GO; GO:0042127; P:regulation of cell proliferation; ISS.

DR InterPro; IPR000152; Asx_hydroxy1_S.

DR InterPro; IPR000152; Asx_hydroxy1_S.

DR InterPro; IPR00074; DSL.

DR InterPro; IPR00074; EGF.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_IT.

DR InterPro; IPR005209; EGF_Like.

DR InterPro; IPR001007; WNF_C.

DR PFAM; PF01414; DSL_1.

DR PFAM; PF000008; EGF_14.

DR PRINTS; PR00010; EGF_BLOOD.

DR SMART; SMD0051; DSL_1.

DR SMART; SMD0079; EGF_Ca; 10.

DR SMART; SMD00214; VWC_1.

DR PS00010; ASX_HYDROXYL; 10.

DR PROSITE; PS00022; EGF_1; 16.

DR PROSITE; PS01186; EGF_2; 12.

DR PROSITE; PS55026; EGF_3; 16.

DR PROSITE; PS00187; EGF_Ca; 8.

KW Calcium-binding; EGF-Like domain; Glycoprotein; Developmental protein; Repeat; Transmembrane; Signal.

PT SIGNAL_1; 33; POTENTIAL.

PT CHAIN_34; 1219; JAGGED_1.

PT DOMAIN_34; 1067; EXTRACELLULAR (POTENTIAL).

PT TRANSMEM_1068; 1093; POTENTIAL.

PT DOMAIN_1094; 1219; CYTOSLAMIC (POTENTIAL).

PT DOMAIN_167; 229; DSU.

PT DOMAIN_230; 266; EGF-LIKE_1 (ATYPICAL).

PT DOMAIN_296; 334; EGF-LIKE_2.

PT DOMAIN_336; 372; EGF-LIKE_3.

PT DOMAIN_374; 410; EGF-LIKE_4; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_412; 448; EGF-LIKE_5; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_450; 485; EGF-LIKE_6; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_487; 523; EGF-LIKE_7; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_525; 561; EGF-LIKE_8.

PT DOMAIN_574; 627; EGF-LIKE_9.

PT DOMAIN_629; 665; EGF-LIKE_10; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_667; 703; EGF-LIKE_11; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_705; 741; EGF-LIKE_12.

PT DOMAIN_744; 780; EGF-LIKE_13.

PT DOMAIN_782; 816; EGF-LIKE_14; CALCIUM-BINDING (POTENTIAL).

PT DOMAIN_820; 856; EGF-LIKE_15; CALCIUM-BINDING (POTENTIAL).

PT DISULFID_300; 312; BY SIMILARITY.

PT DISULFID_306; 322; BY SIMILARITY.

BY SIMILARITY.

DISULFID_324; 333; BY SIMILARITY.

DISULFID_340; 351; BY SIMILARITY.

DISULFID_345; 360; BY SIMILARITY.

DISULFID_362; 371; BY SIMILARITY.

DISULFID_378; 389; BY SIMILARITY.

DISULFID_383; 398; BY SIMILARITY.

DISULFID_400; 409; BY SIMILARITY.

DISULFID_416; 427; BY SIMILARITY.

DISULFID_421; 436; BY SIMILARITY.

DISULFID_438; 447; BY SIMILARITY.

DISULFID_454; 464; BY SIMILARITY.

DISULFID_458; 473; BY SIMILARITY.

DISULFID_475; 484; BY SIMILARITY.

DISULFID_491; 502; BY SIMILARITY.

DISULFID_496; 511; BY SIMILARITY.

DISULFID_513; 522; BY SIMILARITY.

DISULFID_529; 540; BY SIMILARITY.

DISULFID_534; 549; BY SIMILARITY.

DISULFID_551; 560; BY SIMILARITY.

DISULFID_578; 605; BY SIMILARITY.

DISULFID_599; 615; BY SIMILARITY.

DISULFID_617; 626; BY SIMILARITY.

DISULFID_633; 644; BY SIMILARITY.

DISULFID_638; 653; BY SIMILARITY.

DISULFID_655; 664; BY SIMILARITY.

DISULFID_671; 682; BY SIMILARITY.

DISULFID_676; 691; BY SIMILARITY.

DISULFID_693; 702; BY SIMILARITY.

DISULFID_709; 720; BY SIMILARITY.

DISULFID_714; 729; BY SIMILARITY.

DISULFID_731; 740; BY SIMILARITY.

DISULFID_748; 759; BY SIMILARITY.

DISULFID_753; 768; BY SIMILARITY.

DISULFID_770; 779; BY SIMILARITY.

DISULFID_786; 797; BY SIMILARITY.

DISULFID_791; 806; BY SIMILARITY.

DISULFID_808; 817; BY SIMILARITY.

DISULFID_824; 835; BY SIMILARITY.

DISULFID_829; 844; BY SIMILARITY.

DISULFID_846; 855; BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 1219 AA; 134325 MW; 65D4CF23BA0E204 CRC64;

Score 86; DB 1; Length 1219;

Best Local Similarity 27.0%; Pred. No. 0.81; Indels 46; Gaps 9;

Matches 33; Conservative 9; Mismatches 34;

Qy PE---GCTCEVIAAHRC---C-NKRNIBERSQTVKCSCLPGKVACTRNR-----81

Db 325 PEGYSNCE-TAEHAQLSDPCHNRGSCKETSSGFWGTCSINDDCSPNNC 383

Qy 82 ---PSCVDASIVG----KWW-----CEMPCEGLEECKTLPDN-----SG 115

Db 384 SHGGTCQQ-LVNGFKCVCPQWTGKTCOLDANECAKPCYNARSCKNLASYYCDCLPG 441

Qy 116 WM 117

Db 442 WM 443

RESULT 13

ID FBPL_STRPU STANDARD; PRT; 1064 AA.

AC P10079;

DT 01-MAR-1989 (Rel. 10, Created)

01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Fibroplin I precursor (Epidermal growth factor-related protein 1)
 DE (UEGF-1).

GN EGF1.

OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa;
 OC Benthinoidea; Buechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;

OC Strongylocentrotus.
 OX NCBI_TaxID=7668;

RN SEQUENCE FROM N.A.

RP MEDLINE=90112459; PubMed=2514273;

RA Delgadillo-Reynoso M.G.; Rollo D.R.; Hursch D.A.; Raff R.A.;

RT "structural analysis of the UEGF gene in the sea urchin
 Strongylocentrotus purpuratus reveals more similarity to vertebrate
 than to invertebrate genes with EGF-like repeats.";

RT J. Mol. Evol. 29:144-147 (1989).

[2]

RN SEQUENCE OF 279-476 AND 781-1064 FROM N.A.

RP MEDLINE=87319567; PubMed=3198216;

RA Hursch D.A.; Andrews M.E.; Raff R.A.;

RT "A sea urchin gene encodes a polypeptide homologous to epidermal
 growth factor.";

RT Science 237:1487-1490 (1989).

[3]

RN AVIDIN-LIKE DOMAIN.

RP MEDLINE=89196806; PubMed=2784773;

RA Hunt L.T.; Barker W.C.;

RT "avidin-like domain in an epidermal growth factor homolog from a sea
 urchin.";

RL PASEB J. 3:1760-1764 (1989).

[4]

RN RP CHARACTERIZATION.

RP MEDLINE=9128254; PubMed=2060714;

RX Bisgrove B.W.; Andrews M.E.; Raff R.A.;

RA "Fibroplinins," products of an EGF repeat-containing gene, form a
 unique extracellular matrix structure that surrounds the sea urchin
 embryo.";

RT Dev. Biol. 146:89-99 (1991).

CC -!- FUNCTION: Form the apical lamina, a component of the extracellular
 matrix.

CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR. IN VESICLES IN THE CYTOPLASM
 OF UNFERTILIZED EGGS, THEN TO THE BASE OF THE HYALIN LAYER
 THROUGHOUT DEVELOPMENT, AND FINALLY IN THE APICAL LAMINA IN LATE
 EMBRYOS AND EARLY LARVAE.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=IA;

CC IsoID=P10079-1; Sequence=Displayed;

CC Name=IB;

CC IsoID=P10079-2; Sequence=VSP_000451;

CC -!- DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and
 during early cleavage, then rapidly increases in abundance between
 late morula and mesenchyme blastula stages to maximal levels
 maintained through subsequent stages. Expressed both maternally
 and zygotically.

CC -!- SIMILARITY: Contains 21 EGF-like domains.

CC -!- SIMILARITY: Contains 1 CUB domain.

CC -!- SIMILARITY: THE C-TERMINAL DOMAIN OF THIS PROTEIN IS SIMILAR TO
 AVIDIN/STREPPIAVIDIN.

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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license to license@lsb-sib.ch/announce/
 or send an email to license@lsb-sib.ch).

CC EMBL; X17533; CAA35573.1; -

DR PIR; A40136; A4136.

DR HSSP; P01132; IEGF.

DR InterPro; IPR001152; Asx hydroxyl_S.

DR InterPro; IPR000468; Avidin.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR000742; EGF.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR00209; EGF_Like.

PFam; PF00432; Avidin_1.

PFam; PF00431; CUB.

DR PROSITE; PS00010; AVIDIN_1.

DR PRINTS; PR00709; AVIDIN.

SMART; SM00042; CUB_1.

DR PROSITE; SM00179; EGF_CA_20.

DR PROSITE; PS00010; ASX_HYDROXYL_19.

DR PROSITE; PS00577; AVIDIN_1.

DR PROSITE; PS01180; CUB_1.

DR PROSITE; PS00022; EGF_1_19.

DR PROSITE; PS01186; EGF_2_19.

DR PROSITE; PS00026; EGF_3_21.

DR PROSITE; PS01187; EGF_CA_18.

KW Glycoprotein; Alternative splicing; EGF-like domain, Repeat; Signal;

FT SIGNAL_1 1 19 POTENTIAL.

FT CHAIN 20 1064 FIBROPLIN_I.

FT DOMAIN 20 55 EGF-LIKE_1.

FT DOMAIN 62 175 CUB.

FT DOMAIN 176 212 EGF-LIKE_2.

FT DOMAIN 214 250 EGF-LIKE_3.

FT DOMAIN 252 288 EGF-LIKE_4.

FT DOMAIN 290 326 EGF-LIKE_5.

FT DOMAIN 328 364 EGF-LIKE_6.

FT DOMAIN 366 402 EGF-LIKE_7.

FT DOMAIN 404 440 EGF-LIKE_8.

FT DOMAIN 442 478 EGF-LIKE_9.

FT DOMAIN 480 516 EGF-LIKE_10.

FT DOMAIN 518 554 EGF-LIKE_11.

FT DOMAIN 556 592 EGF-LIKE_12.

FT DOMAIN 594 630 EGF-LIKE_13.

FT DOMAIN 632 668 EGF-LIKE_14.

FT DOMAIN 670 706 EGF-LIKE_15.

FT DOMAIN 708 744 EGF-LIKE_16.

FT DOMAIN 746 782 EGF-LIKE_17.

FT DOMAIN 784 820 EGF-LIKE_18.

FT DOMAIN 822 858 EGF-LIKE_19.

FT DOMAIN 860 896 EGF-LIKE_20.

FT DOMAIN 898 934 EGF-LIKE_21.

FT DOMAIN 936 1064 CALCIUM-BINDING (POTENTIAL).

FT DISULFID 23 34 BY SIMILARITY.

FT DISULFID 28 43 BY SIMILARITY.

FT DISULFID 45 54 BY SIMILARITY.

FT DISULFID 180 191 BY SIMILARITY.

FT DISULFID 185 200 BY SIMILARITY.

FT DISULFID 202 211 BY SIMILARITY.

FT DISULFID 218 229 BY SIMILARITY.

FT DISULFID 223 238 BY SIMILARITY.

FT DISULFID 240 249 BY SIMILARITY.

FT DISULFID 256 267 BY SIMILARITY.

FT DISULFID 261 276 BY SIMILARITY.

FT DISULFID 278 287 BY SIMILARITY.

FT DISULFID 294 305 BY SIMILARITY.

FT DISULFID 299 314 BY SIMILARITY.

FT DISULFID 316 325 BY SIMILARITY.

FT DISULFID 332 343 BY SIMILARITY.

FT DISULFID 337 352 BY SIMILARITY.

FT DISULFID 354 363 BY SIMILARITY.

FT DISULFID 370 381 BY SIMILARITY.

FT DISULFID 375 390 BY SIMILARITY.

GN	NOTCH4.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates;
NCBI_TAXID	9606;
RN	
[1]	SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-L-EW. SEQUENCE FROM PLACENTA; TISSUE=PLACENTA; MEDLINE=9713116; PubMed=9168133;
[2]	SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). SEQUENCE FROM BONE marrow, and Heart; TISSUE=BONE marrow; PubMed=9168133; MEDLINE=93160091; PubMed=9693032;
[3]	SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317. Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.; "Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3."; Gene 189:235-244 (1997).
[4]	IDENTIFICATION OF LIGANDS. SEQUENCE=9180765; PubMed=1007256;
[5]	FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May regulate branching morphogenesis in the developing vascular system (By similarity). SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).
[6]	SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
[7]	ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Comment=Experimental confirmation may be lacking for some isoforms; Name=1; Isoform=Q99466-1; Sequence=Displayed;
[8]	Name=2; Isoform=Q99466-2; Sequence=VSP_001406;
[9]	Name=3; Isoform=Q99466-3; Sequence=VSP_001407;
[10]	- - TISSUE SPECIFICITY: Highly expressed in the heart, moderately in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or peripheral blood leukocytes.
[11]	PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a NOTCH-derived peptide containing the intracellular domain (NICD).

from the membrane (By similarity).

-|- PIM: Phosphorylated (By similarity).

-|- POLYMORPHISM: The Poly-Leu region of NOTCH4 (in the signal peptide) is polymorphic and the number of Leu varies in the population (from 6 to 12).

-|- SIMILARITY: Belongs to the NOTCH family.

-|- SIMILARITY: Contains 28 EGF-like domains

-|- SIMILARITY: Contains 3 Lin/Notch repeats.

-|- SIMILARITY: Contains 5 ANK repeats.

-|- CAUTION: Ref_1 sequence differs from that shown due to frameshifts in position 1438 to 1463.

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EMBL; D63395; BAA09701; ALT_FRAME.

EMBL; D86566; BAA13116; 1;

EMBL; U95299; AAC32288; 1;

EMBL; U89335; AAC63097; 1;

EMBL; AB023967; BA020317; 1;

EMBL; AB024520; BA088951; 1;

EMBL; AB055778; BA088952; 1;

HSSP; P08709; 1BF9.

GenBank: HGNC:7884; NOTCH4.

MTM; 164951; -.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000152; ASX_hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR01881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_Like.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR002977; Notch.

DR InterPro; IPR000800; Notch_dom.

Pfam; PF00033; Notch;

Pfam; PF00008; EGF;

Pfam; PF00066; notch;

Pfam; PF000279; Notch_1.

PRINTS; PR00010; EGBLOOD.

PRINTS; PR00011; EGFLAMININ.

PRINTS; PR01422; NOTCH.

SMART; SM00248; ANK; 5.

SMART; SM00179; EGF_CA; 11.

SMART; SM00004; NL_3.

PROSITE; PS50297; ANK REP REGION; 1..

PROSITE; PS50088; ANK REPEAT; 5..

PROSITE; PS00010; ASX_HYDROXYL; 11..

PROSITE; PS00022; EGF_1; 28..

PROSITE; PS01186; EGF_2; 21..

PROSITE; PS50026; EGF_3; 28..

PROSITE; PS01187; EGF_CA; 9..

DR Receptor; Transcription regulation, Activator; Differentiation;

KW Developmental protein; Repeat; ANK repeat; EGF-like domain;

KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;

KW Triplet repeat expansion; Alternative splicing.

SIGNAL; 1 23 POTENTIAL_EXTRACELLULAR (POTENTIAL).

FT DOMAIN; 24 1447 POTENTIAL.

FT TRANSMEM DOMAIN; 1448 1468 POTENTIAL.

FT DOMAIN; 1469 2003 CYTOPLASMIC (POTENTIAL).

FT DOMAIN; 24 63 NOTCH EXTRACELLULAR TRUNCATION (BY SIMILARITY).

FT DOMAIN; 64 115 NOTCH INTRACELLULAR DOMAIN (BY SIMILARITY).

FT DOMAIN; 118 155 NOTCH EXTRACELLULAR (POTENTIAL).

FT DOMAIN; 156 192 NOTCH EXTRACELLULAR (POTENTIAL).

	RESULT 15	JAG2 MOUSE	STANDARD;	PRT;	1247 AA.
ID	JAG2 MOUSE				
AC	Q9QB5; M139; 07-01-19;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DR	JAG2_2 (precursor) (Unmodified)				
Query Match	11.2%; Score 84.5; DB 1; Length 2003;				
Best Local Similarity	31.0%; Pred. No. 1.9;				
Matches	39; Conservative 6; Mismatches 42; Indels 39; Gaps				
Qy	18 CAMLICH-GS---LQHPTFQKQHHLRP---BGGTCVY---IAHRCNCNKRBEERSQTVK				
Db	479 CLSQPCPCHPSOTCLDLRNF---HCLCPGQIEQQLCEVETNECASCAPUNHADCHDLINGQ				
Qy	67 CSQLPKVAGTTRNRSPC---VDASIVIGKWWNCEMPEPLEGB---				-CKTLPDNS
Db	537 CICDPG-FSGT---RCBEDIDE-----CRSSSPCANGGOCQDQPGAFHCKCPLGFE				
Qy	115 GMGAT 120				
Db	583 GPRCQT 588				

JAG2.
Mus musculus (Mouse).
Submitted (DBC-1997) to the EMBL/GenBank/DDBJ databases.

[12]
SEQUENCE OF 302-819 FROM N.A.

RC TISSUE-Brain;
RX MEDLINE=98051918; PubMed=9341252;
RA Lan Y.; Jiang R.; Shawber C.; Weinmaster G.; Gridley T.;
RT "The Jagged2 gene maps to chromosome 12 and is a candidate for the lgl
and sm mutations";
RL Mamm. Genome 8:875-876 (1997).

[3]
RN SEQUENCE OF 325-759 FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=98145947; PubMed=9486542;
RA Iuso B.; Aster J.C.; Hasserian R.P.; Kuo F.; Sklar J.;
RT "Isolation and functional analysis of cDNA for human Jagged2, a gene
encoding a ligand for the Notch receptor.";
RL Mol. Cell. Biol. 17:6057-6067 (1997).

CC -!- FUNCTION: Putative Notch ligand involved in the mediation of Notch
signaling. Plays an essential role during limb, craniofacial and
thymic development. May be involved in myogenesis and in the
development of peripheral and central nervous systems.

CC -!- TISSUE-SPECIFICITY: Found to be highest in fetal thymus,
epidermis, foregut dorsal root ganglia and inner ear. In 2-week-old
mice, abundant in heart, lung, thymus, skeletal muscle, brain
and testis. Expression overlaps partially with Notch1 expression.

CC -!- DEVELOPMENTAL STAGE: At 13 dpc, found in paravertebral vessels and
dorsal root ganglia. At 14 dpc, in oropharyngeal epithelium,
developing thymus and in the muscles of the tongue. By 15 dpc, in
many tissues

CC -!- SIMILARITY: Contains 16 EGF-like domains.

CC -!- SIMILARITY: Contains 1 DSL domain.

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CC DR EMBL; AF038572; AAF16411.1; -.
DR EMBL; Y14495; CAA74835.1; -.
DR HSSP; P00743; 1CCOF.
DR MGD; MGI:1098270; Jag2.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005112; F:growth factor activity; ISS.
DR GO; GO:0010137; AAC14010.1; -.
DR GO; GO:0010749; P:Notch binding; IPI.
DR GO; GO:0030154; P:cell cycle; ISS.
DR GO; GO:0010109; P:cell fate determination; NAS.
DR GO; GO:0010747; P:cell-cell signaling; NAS.
DR GO; GO:0042492; P:gamma-delta T-cell differentiation; IMP.
DR GO; GO:0009912; P:hair cell fate commitment; IMP.
DR GO; GO:0010765; P:hearing; NAS.
DR GO; GO:0030326; P:limb morphogenesis; ISS.

GO; GO:0007219; P:N signaling pathway; ISS.
GO; GO:000334; P:regulation of cell migration; ISS.
DR GO; GO:0042127; P:regulation of cell proliferation; ISS.
DR GO; GO:0007283; P:spermatogenesis; ISS.
GO; GO:0045061; P:thymic T-cell selection; ISS.
InterPro; IPR001152; ASX_hydroxy_S.
InterPro; IPR001774; DSL.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_2A.
InterPro; IPR001438; EGF_I.I.
InterPro; IPR006209; EGF_Like.
InterPro; IPR001007; WWF_-.
PFam; PF01414; DSL; 1.
PFam; PF00008; EGE; 14.
PRINTS; PRO0010; EGPBLLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 9.
PROSITE; PS00010; ASX_HYDROXYL; 10.
PROSITE; PS00022; VWC; 1.
PROSITE; PS00051; EGF2; 16.
PROSITE; PS01186; EGF2; 15.
PROSITE; PS50028; EGF_3; 15.
PROSITE; PS01187; EGF_CA; 7.
KW Calcium-binding; EGF_Like domain; Glycoprotein; Developmental protein;
repeat; Signal; Transmembrane.
SIGNAL 1 23
FT CHAIN 24 1247
FT DOMAIN 24 1084
FT TRANSMEM 24 107
FT DOMAIN 1108 1107
FT DOMAIN 1108 1247
FT DOMAIN 178 240
FT DOMAIN 241 274
FT DOMAIN 275 305
FT DOMAIN 307 345
FT DOMAIN 347 383
FT DOMAIN 385 421
FT DOMAIN 423 459
FT DOMAIN 461 496
FT DOMAIN 498 534
FT DOMAIN 536 572
FT DOMAIN 574 634
FT DOMAIN 636 672
FT DOMAIN 674 710
FT DOMAIN 712 748
FT DOMAIN 751 787
FT DOMAIN 789 825
FT DISULFID 827 863
FT DISULFID 245 256
FT DISULFID 249 262
FT DISULFID 264 273
FT DISULFID 276 287
FT DISULFID 282 293
FT DISULFID 295 304
FT DISULFID 311 323
FT DISULFID 317 333
FT DISULFID 335 344
FT DISULFID 351 362
FT DISULFID 356 371
FT DISULFID 373 382
FT DISULFID 389 400
FT DISULFID 394 409
FT DISULFID 411 420
FT DISULFID 427 438
FT DISULFID 432 447
FT DISULFID 449 458
FT DISULFID 465 475
FT DISULFID 469 484
FT DISULFID 486 495
FT DISULFID 502 513
FT DISULFID 507 522
FT DISULFID 524 533
FT DISULFID 540 551
FT DISULFID 545 560

FT DISULFID 562 BY SIMILARITY.
 FT DISULFID 589 612 POTENTIAL.
 FT DISULFID 606 622 BY SIMILARITY.
 FT DISULFID 624 633 BY SIMILARITY.
 FT DISULFID 640 651 BY SIMILARITY.
 FT DISULFID 645 660 BY SIMILARITY.
 FT DISULFID 662 671 BY SIMILARITY.
 FT DISULFID 678 689 BY SIMILARITY.
 FT DISULFID 683 698 BY SIMILARITY.
 FT DISULFID 700 709 BY SIMILARITY.
 FT DISULFID 716 727 BY SIMILARITY.
 FT DISULFID 721 736 BY SIMILARITY.
 FT DISULFID 738 747 BY SIMILARITY.
 FT DISULFID 755 766 BY SIMILARITY.
 FT DISULFID 760 775 BY SIMILARITY.
 FT DISULFID 777 786 BY SIMILARITY.
 FT DISULFID 793 804 BY SIMILARITY.
 FT DISULFID 798 813 BY SIMILARITY.
 FT DISULFID 815 824 BY SIMILARITY.
 FT DISULFID 831 842 BY SIMILARITY.
 FT DISULFID 836 851 BY SIMILARITY.
 FT DISULFID 853 862 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 570 570 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 619 619 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 752 752 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1060 1060 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 302 302 L -> M (IN REF. 2).
 FT CONFLICT 461 461 N -> T (IN REF. 2).
 FT CONFLICT 469 478 CORGTCKDL -> VSANGLQGP (IN REF. 2).
 FT CONFLICT 492 492 G -> V (IN REF. 2).
 FT CONFLICT 546 546 L -> F (IN REF. 2).
 FT CONFLICT 549 549 A -> V (IN REF. 2).
 FT CONFLICT 735 738 RCAC -> PAR (IN REF. 3).
 FT CONFLICT 809 809 N -> H (IN REF. 2).
 FT CONFLICT 812 812 R -> A (IN REF. 2).
 SQ SEQUENCE 1247 AA; 134726 MW; 1D80C8626FAFABEC CRC64;
 Qy CHSGLQHTFQQHHLDHRPBEGTC-EVIAAHRG-----CNRKRI- 58
 Db 465 CHSOQCH-----GGTCDLVNGYQCVRPRGFGRHCELEYDKASSPBRGGIC 513
 Qy 23 EERSQTVKCSCLPGKVAGTTNRPSC-YDASIVIGKWCMEPCLEGEBCKTLPDNSGWM 117
 Qy 59 EDLYDGFRCHC-PRLGSLG-----HCEVDMDL----CEPSPLNGRCYNL--EGDYY 559
 Qy 118 CA 119
 Db 560 CA 561

Query Match 11.1%; Score 84; DB 1; Length 124;

Best Local Similarity 24.6%; Pred. No. 1.3; Matches 30; Conservative 12; Mismatches 30; Indels 50; Gaps 9;

Qy CHSGLQHTFQQHHLDHRPBEGTC-EVIAAHRG-----CNRKRI- 58

Db 465 CHSOQCH-----GGTCDLVNGYQCVRPRGFGRHCELEYDKASSPBRGGIC 513

Qy 23 EERSQTVKCSCLPGKVAGTTNRPSC-YDASIVIGKWCMEPCLEGEBCKTLPDNSGWM 117

Db 514 EDLYDGFRCHC-PRLGSLG-----HCEVDMDL----CEPSPLNGRCYNL--EGDYY 559

Search completed: April 8, 2004, 13:16:40
 Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2004, 13:15:04 ; Search time 22 Seconds
(without alignments)
312.102 Million cell updates/sec

Title: US-09-763-335-2

Perfect score: 754

Sequence: 1 MAMYSAMSIVTYLWISACAM.....SGHMCATGNKIKTRIHPRT 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:^{*}

1: /cgmn2_6/_ptodata/2/iaa/5A_COMB.pep:
2: /cgmn2_6/_ptodata/2/iaa/5B_COMB.pep:
3: /cgmn2_6/_ptodata/2/iaa/6A_COMB.pep:
4: /cgmn2_6/_ptodata/2/iaa/6B_COMB.pep:
5: /cgmn2_6/_ptodata/2/iaa/PCTUS_COMB.pep:
6: /cgmn2_6/_ptodata/2/iaa/backfile1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	150	19.9	29	US-09-905-223-451	Sequence 451, App
2	110.5	14.7	1248	3	Sequence 6, App
3	96	12.7	1964	4	Sequence 1, App
4	91.5	12.1	233	4	Sequence 110, App
5	86.5	11.5	156	4	Sequence 22898, A
6	86.5	11.5	1139	1	Sequence 4, App
7	86.5	11.5	1139	3	Sequence 4, App
8	86.5	11.5	2703	1	Sequence 19, App
9	86.5	11.5	2703	4	Sequence 4, App
10	86	11.4	500	4	Sequence 2, App
11	86	11.4	659	4	Sequence 3, App
12	86	11.4	685	3	Sequence 2, App
13	86	11.4	685	3	Sequence 25, App
14	86	11.4	1010	3	Sequence 7, App
15	86	11.4	1036	4	Sequence 6, App
16	86	11.4	1187	4	Sequence 7, App
17	86	11.4	1208	4	Sequence 1, App
18	86	11.4	1218	2	Sequence 6, App
19	86	11.4	1218	3	Sequence 6, App
20	86	11.4	1218	3	Sequence 2, App
21	86	11.4	1218	3	Sequence 7, App
22	86	11.4	1218	4	Sequence 11, App
23	86	11.4	1218	4	Sequence 7, App
24	86	11.4	1219	3	Sequence 5, App
25	84	11.1	2523	4	Sequence 18, App
26	84	11.1	2523	4	Sequence 3, App
27	82.5	10.9	2471	1	Sequence 16, App

389414

ALIGNMENTS

RESULT 1

US-09-905-223-451

; Sequence 451, Application US/08905223

; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.

; APPLICANT: Duebert, Aymeric Bruno

; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Win95

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/905, 223

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelien, Ned A.

; REGISTRATION NUMBER: 23, 655

; REFERENCE DOCUMENT NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 235-8550

; TELEFAX: (619) 235-0176

; INFORMATION FOR SEQ ID NO: 451:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 29 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

; ORIGINAL SOURCE: Homo Sapiens

; TISSUE TYPE: Brain

; FEATURE:

; NAME/KEY: big peptide

; LOCATION: -25,-1

; IDENTIFICATION METHOD: Von Heijne matrix

; OTHER INFORMATION: score 5.8

; OTHER INFORMATION: seq LWISACMILCHG/SL

; US-08-905-223-451

Query Match 19.9%; Score 150; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred. No. 1.9e-09;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAMVSAMSWVLYLWISACMLLCHGSLQ 28
 Db 1 MAMVSAMSWVLYLWISACMLLCHGSLQ 28

RESULT 2
 US-08-882-046-6
 Sequence 6, Application US/08882046
 ; Patent No. 6136952
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Linheng
 ; APPLICANT: Hood, Leroy
 ; APPLICANT: Krantz, Ian D.
 ; APPLICANT: Spinner, Nancy B.
 ; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
 ; TITLE OF INVENTION: Nucleic Acids and Methods of Use
 ; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 3470 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/882,046
 ; FILING DATE: 25-JUN-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Kathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UW 2637
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-9949
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1248 amino acids
 ; TYPE:
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: peptide
 US-08-882-046-6

Query Match 14.7%; Score 110.5; DB 3; Length 1248;
 Best Local Similarity 27.0%; Pred. No. 0.0022;
 Matches 33; Conservative 13; Mismatches 27; Indels 49; Gaps 9;

Qy 23 CHGSLQHTEQQHHLHRPEGSTC-EVIAAHR-C-----CNKNR1- 58
 Db 465 CHGQCOH-----GETCKDOLVNGYOCVCPRGFGRHCELEYKKCASSPQRGGIC 513

Qy 59 EERSQTVKCSCLPGKVAGTRNRPAC-VDAASIVGKWWCMEPCLEGEEKTLPDNSGMM 117
 Db 514 EDLVDGFRCH- PRGUSG----PLCEVDL-----WCPNPCLNGARCYNLED--'YY 560

Qy 118 CA 119
 Db 561 CA 562

RESULT 3
 US-09-467-997-1
 Sequence 1, Application US/09467997
 ; Patent No. 6379925

Query Match 12.7%; Score 96; DB 4; Length 1964;
 Best Local Similarity 26.8%; Pred. No. 0.13;
 Matches 33; Conservative 8; Mismatches 48; Indels 34; Gaps 6;

Qy 15 ISACMLIC-HGSLOHQTFQOHHHLHRPRGGTC-----EVIAAHR--CCNKNR1 58
 Db 689 LGCCISTSPCAHGCTCP-----QPGYGNCTCPAGMGLTSEEVTAChGPCLNGGSC 741

Qy 59 EERSQTVKCSCLPGKVAGTRNRPSCDASIVGKWWCMEPCLEGEEKTLPDNSGMM 118
 Db 742 SIRPEGYSCTCLP--SHTGRHCQTAVD-----HCVSASCLNGCTVNGKPGTPCLC 790

Qy 119 ATG 121
 Db 791 ATG 793

RESULT 4
 US-09-216-393B-110
 ; Sequence 110, Application US/09216393B
 ; Patent No. 6514694
 ; GENERAL INFORMATION:
 ; APPLICANT: Milhausen, Michael James
 ; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEAR ACID MOLECULES, AND USES THEREOF
 ; FILE REFERENCE: TX-1-C2
 ; CURRENT APPLICATION NUMBER: US/09/216,393B
 ; PRIORITY APPLICATION NUMBER: 08-12-18
 ; PRIOR APPLICATION NUMBER: 08-994,825
 ; PRIORITY FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 366
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 110
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Toxoplasma gondii
 US-09-216-393B-110

Query Match 12.1%; Score 91.5; DB 4; Length 233;
 Best Local Similarity 25.9%; Pred. No. 0.036;
 Matches 28; Conservative 6; Mismatches 39; Indels 35; Gaps 4;

Qy 18 CAMLICLGSLSQHTEQQHHLHRPEGSTC-EVIAHRC-----CNKRN-----RIBERS 62
 Db 78 CQCDACHG-----GKTCTTKCINCINDSDCNGHGTNTNCNTERGF 122

Qy 63 QTVKCSCLPGKVAGTRNRPSCDASIVGKWWCMEPCLEGEEKTL 110
 Db 123 AGTNCSSSGKCSKT-----CLSGHNPATGACVCDPCTHGRCTL 165

RESULT 5
 US-09-252-991A-22898
 ; Sequence 22898, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS.: 33142
 SEQ ID NO: 22898
 LENGTH: 156
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-91A-22898

Query Match 11.5%; Score 86.5; DB 1; Length 1139;
 Best Local Similarity 25.9%; Pred. No. 0.74; Indels 19; Gaps 3;
 Matches 22; Conservative 10; Mismatches 34; Query Match 83
 Qy 40 EGGTCEV----IAAHCCNKRRIEERSQTVCLPGKVA-----GTTTNRPS 83
 Db 26 QGQNCEINIDDCAPNPQNGTCTDRMANFCSCPPTGMGLICEINKDDCKPGACINGS 85

Query Match 11.5%; Score 86.5; DB 4; Length 156;
 Best Local Similarity 25.0%; Pred. No. 0.078; Indels 23; Gaps 5;
 Matches 32; Conservative 9; Mismatches 64; Query Match 65
 Qy 6 AMSWVLWISACAMLLCHGSLSLTHFOGHHLRPEGGTCEVIAAHRCNKRRIEERSQTV 65
 Db 12 ARSW-XWSWAS-TSTGCLDTYAPARRSPARGSSKAVIARRCNCATPCNSRSP 67

RESULT 7 US-09-113-825-4

Sequence 4, Application US/09113825
 Patent No. 6149902

GENERAL INFORMATION:
 APPLICANT: Aravanis-Tsakonas, Spyridon
 ATTORNEY/AGENT: Fortini, Mark
 TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1115 Avenue of the Americas
 CITY: New York
 STATE: NY
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113,825
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/537,210
 FILING DATE: 29-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-750-9050
 TELEFAX: 212-869-8864
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Dros N
 LOCATION: 1189 . . . 2327
 OTHER INFORMATION: Highly conserved ankyrin repeat
 US-09-113-825-4

Query Match 11.5%; Score 86.5; DB 3; Length 1139;

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS.: 33142
 SEQ ID NO: 22898
 LENGTH: 156
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-91A-22898

Query Match 11.5%; Score 86.5; DB 1; Length 1139;
 Best Local Similarity 25.9%; Pred. No. 0.74; Indels 19; Gaps 3;
 Matches 22; Conservative 10; Mismatches 34; Query Match 83
 Qy 40 EGGTCEV----IAAHCCNKRRIEERSQTVCLPGKVA-----GTTTNRPS 83
 Db 26 QGQNCEINIDDCAPNPQNGTCTDRMANFCSCPPTGMGLICEINKDDCKPGACINGS 85

Query Match 11.5%; Score 86.5; DB 4; Length 156;
 Best Local Similarity 25.0%; Pred. No. 0.078; Indels 23; Gaps 5;
 Matches 32; Conservative 9; Mismatches 64; Query Match 65
 Qy 6 AMSWVLWISACAMLLCHGSLSLTHFOGHHLRPEGGTCEVIAAHRCNKRRIEERSQTV 65
 Db 12 ARSW-XWSWAS-TSTGCLDTYAPARRSPARGSSKAVIARRCNCATPCNSRSP 67

RESULT 7 US-09-113-825-4

Sequence 4, Application US/09113825
 Patent No. 6149902

GENERAL INFORMATION:
 APPLICANT: Aravanis-Tsakonas, Spyridon
 ATTORNEY/AGENT: Fortini, Mark
 TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1115 Avenue of the Americas
 CITY: New York
 STATE: NY
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113,825
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/537,210
 FILING DATE: 29-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-750-9050
 TELEFAX: 212-869-8864
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Dros N
 LOCATION: 1189 . . . 2327
 OTHER INFORMATION: Highly conserved ankyrin repeat
 US-09-113-825-4

Query Match 11.5%; Score 86.5; DB 3; Length 1139;

CURRENT FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-3

RESULT 13
US-09-423-753-25
; Sequence 25: Application US/09423753
; Patent No. 666409
; GENERAL INFORMATION:
; APPLICANT: SAKANO, SEIJI
; TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
; FILE REFERENCE: KP-8693
; CURRENT APPLICATION NUMBER: US/09/423 , 753
; CURRENT FILING DATE: 1999-12-30
; PRIORITY NUMBER: PCT/JP98/02104
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 9/124064
; PRIOR FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 25
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-25

Query Match Score 86; DB 4; Length 659;
Best Local Similarity 25.0%; Pred. No. 0.45; Indels 30; Gaps 6;
Matches 28; Conservative 9; Mismatches 45;

Qy 14 WISAC---AMLLCHGSLQHTFOQHHLRPEGGTCEVIAAHRCCNKRRIERSQTVKSC 69
Db 242 WQCTCDEGMGLFCQDQANYC--THHSPCKNGATC-----SNSGQRSYT--CTC 286

Qy 70 LPGKVAGITTRNRPSCVDASTIVIGRWCMEPCLEGECKTLPDNSGMCATG 121
Db 287 RPYTG-----VDCELELSE--CDSNPCKRNGGSKDQEDGYHCLCPG 327

RESULT 12
US-08-872-855-2
; Sequence 2: Application US/08872855
; Patent No. 6121045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REFFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match Score 86; DB 3; Length 685;
Best Local Similarity 25.0%; Pred. No. 0.47; Indels 30; Gaps 6;
Matches 28; Conservative 9; Mismatches 45;

Qy 14 WISAC---AMLLCHGSLQHTFOQHHLRPEGGTCEVIAAHRCCNKRRIERSQTVKSC 69
Db 313 RPYTG-----VDCELELSE--CDSNPCKRNGGSKDQEDGYHCLCPG 353

RESULT 14
US-08-882-046-7
; Sequence 7: Application US/08882046
; Patent No. 6116952
; GENERAL INFORMATION:
; APPLICANT: Li Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Kraatz, Ian D.
; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UW 2637
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1010 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-882-046-7

Query Match 11.4%; Score 86; DB 3; Length 1010;
 Best Local Similarity 23.8%; Pred. No. 0.73;
 Matches 34; Conservative 11; Mismatches 34; Indels 64; Gaps 9;
 Qy 37 HRP-EGGTCE-----VIAAHRC---C-NKNRRIERSQTVKSC 69
 Db 303 HQPCLNGTCSNTGPDKYQCSCPGYSGPNCETAEHACLSDPCHNRGSCKETSLGFEC 362
 Qy 70 LPGKVAGTTRN-----PSCYDASIVG----KWW-----CEMEP 100
 Db 363 SPWTGPTCSTNIDDCSPNNCSHGGTCQD-LVNGFKCVCPQWTGKTCQLDANECEAKP 420
 Qy 101 CLEGECKTLPDN-----SGWM 117
 Db 421 CNAKSKCNLIAAYCDLPGWM 443

RESULT 15
 US-09-068-740A-6
 Sequence 6, Application US/09068740A
 ; Patent No. 6337387
 ; GENERAL INFORMATION:
 ; APPLICANT: SAKANO, SETUJI
 ; ATTORNEY: ITOH, AKIRA
 ; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
 ; FILE REFERENCE: KP-8447
 ; CURRENT APPLICATION NUMBER: US/09/068,740A
 ; CURRENT FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: JP 7-299611
 ; PRIOR FILING DATE: 1995-11-17
 ; PRIOR APPLICATION NUMBER: JP 7-311811
 ; PRIOR FILING DATE: 1995-11-30
 ; PRIOR APPLICATION NUMBER: PCT/JP96/03356
 ; PRIOR FILING DATE: 1996-11-15
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 1036
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-068-740A-6

Query Match 11.4%; Score 86; DB 4; Length 1036;
 Best Local Similarity 23.8%; Pred. No. 0.75;
 Matches 34; Conservative 11; Mismatches 34; Indels 64; Gaps 9;
 Qy 37 HRP-EGGTCE-----VIAAHRC---C-NKNRRIERSQTVKSC 69
 Db 272 HQPCLNGTCSNTGPDKYQCSCPGYSGPNCETAEHACLSDPCHNRGSCKETSLGFEC 331
 Qy 70 LPGKVAGTTRN-----PSCYDASIVG----KWW-----CEMEP 100
 Db 332 SPWTGPTCSTNIDDCSPNNCSHGGTCQD-LVNGFKCVCPQWTGKTCQLDANECEAKP 389
 Qy 101 CLEGECKTLPDN-----SGWM 117
 Db 390 CNAKSKCNLIAAYCDLPGWM 412

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OM protein - protein search, using sw model

Run on: April 8, 2004, 13:14:59 ; Search time 20 Seconds

(without alignments)
639 674 Million cell updates/secTitle: US-09-763-335-2
Perfect score: 754
Sequence: 1 MAMYSAMSATLYLNISACAM.....SGWMCATGNKIKTRIHPRT 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	14.1	3871	2 T22812	hypothetical protein notch4 - mouse
2	96	12.7	1964	2 T09059	notch-1 protein homo
3	95	12.7	2531	2 S18188	notch-1 protein -
4	95	12.7	2531	2 A46019	Notch homolog prot
5	94.5	12.5	2352	2 T30201	notch homolog - se
6	93	12.3	2531	2 T31072	crumbs protein - f
7	92.5	12.3	2139	2 A356772	notch protein - fr
8	86.5	11.5	2703	1 A244220	Delta-4 protein -
9	86	11.4	685	2 J7570	jaggedged protein pre
10	86	11.4	1220	2 A56136	fibropallin ta - b
11	85.5	11.3	1064	2 A40126	Xotch protein - Af
12	84	11.1	2524	2 A35844	Motch B protein -
13	82.5	10.9	1203	2 A49175	cell-fate determin
14	82.5	10.9	2471	2 A49128	notch 3 protein - h
15	82	10.9	2318	2 S43056	neurogenic repeatit
16	82	10.9	4544	1 S02392	disintegrin and me
17	82	10.9	5376	2 T42215	metalloproteinase
18	81.5	10.8	355	2 S56058	Notch homolog Motc
19	81.5	10.8	2555	2 A40043	hypothetical prote
20	81	10.7	907	2 T27317	notch3 protein -
21	80.5	10.7	2321	2 S78549	neurogenic repetit
22	79	10.5	293	2 B26637	disintegrin and me
23	79	10.5	655	2 JC7850	metalloproteinase
24	79	10.5	660	2 S71949	Notch homolog Motc
25	79	10.5	861	2 A48825	hypothetical prote
26	78.5	10.4	502	2 T20150	thrombospondin pre
27	78.5	10.4	838	2 T20125	MEGF2 protein - hu
28	78.5	10.4	1178	1 A39804	submitted to the EMBL Data Library, October 1997
29	78.5	10.4	1364	2 T00250	

RESULT 1

T22812

hypothetical protein ZC116.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_change 15-Oct-1999

C;Accession: T22812; 127494

R;Burton, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19618

A;Accession: T22812

A;Status: preliminary; translated from GB/EMBL/DDB/J

A;Molecule type: DNA

A;Residues: 1-3871 <WIL>

A;Cross-references: ENBL:274473; PIDN:CAA989557.1; GSPDB:GN00023; CESP:ZC116.3

A;Experimental source: Clone F56H9

R;Smee, R.

submitted to the EMBL Data Library, June 1996

A;Reference number: 220376

A;Accession: T27494

A;Status: preliminary; translated from GB/EMBL/DDB/J

A;Molecule type: DNA

A;Residues: 1-3871 <WIL>

A;Cross-references: ENBL:2740446; PIDN:CAA98557.1; GSPDB:GN00023; CESP:ZC116.3

A;Experimental source: Clone ZC116

A;Accession: T220376

A;Status: preliminary; translated from GB/EMBL/DDB/J

C;Genetics:

A;Gene: CESP:ZC116.3

A;Map position: 5

A;Introns: 29/3; 66/2; 244/1; 359/3; 422/1; 549/1; 572/1; 728/1; 820/1; 889/3; 1189/1; 1

C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

Query Match 14.1t: Score 106; DB 2; Length 3871;

Best Local Similarity 31.2t: Pred. No. 0.069; No. of Mismatches 40; Indels 22; Gaps 6;

Matches 34; Conservative 13; Mismatches 13;

OY 24 HGSIQLTHQQHHHLHRPREGTCVIAAPCCNNRERPSQ----TVYKCSCLPGKAGT 77

14.8 HGSI----CQYIMSA-C-SKTFELCGPGHCITSVIDPTGQSSSDTTRTKYCICDWBGFVSS 202

QY 78 TRURPSCYDASIVGKWCMEPCLEGBCKLPDN--SGWNMCATONK 123

Db 203 DRNPNTCYDVN----ECESPCPHCYDNCIPGSCFVCSSG-CPKYK 243

C;Species: Mus musculus (house mouse)

C;Date: 11-Jun-1999 #sequence_change 11-Jun-1999

C;Accession: T09059

R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.B.; Dankers, C.; Loretz, C.; Sc

A;Description: Sequence of the mouse major histocompatibility locus class III region.

A;Reference number: Z16543

A;Accession: T0959

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1964 <ROW>

A;Cross-references: EMBL:AP030001; NID:g2564945; PMID:92564945

C;Genetics:

A;Gene: notchA

A;Map position: 17

A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67169/3; 1729/1; 1761/3

C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

C;Keywords: receptor; signal transduction

F;514-545/Domain: EGF homology <EGF>

Query Match Score 96; DB 2; Length 1964;

Best Local Similarity 26.8%; Pred. No. 0.34;

Matches 33; Conservative 8; Mismatches 48; Indels 34; Gaps 6;

Qy 15 ISACAMILCHGSLQHTPQQHHHLRPESGTC-----EVAAHR--CCNKRRI 58

Db 689 LGCCISTPRAHGTCHP-----QPSGYNCTCPAGYNGLTCSBEVTAACHSGPCLNGSC 741

Qy 59 ERSQTVKCSCLPKVKAGTTRNPRSPCVDAISIVGKWWCEMPLEGECKTLPDNSGEMC 118

Db 742 SIREPGYSTCLP-----SHTGHCQTAVD-----HCVSASCINGTQVNKGTFFCOL 790

Qy 119 ATG 121

Db 791 ATG 793

RESULT 3

S18188

notch protein homolog - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: S18188

R;Weinmaster, G.; Roberts, V.J.; Lemke, G.

A;Development: 11.3 - 19.25, 1991

A;Title: A homolog of Drosophila Notch expressed during mammalian development.

A;Reference number: S18188; MUID:92111383; PMID:1764995

A;Accession: S18188

A;Molecule type: mRNA

A;Residues: 1-2531 <WEL>

A;Cross-references: EMBL:X57405; NID:g57634; PMID:957634

C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

F;987-1018/Domain: EGF homology <EGF1>

F;1025-1056/Domain: EGF homology <EGF2>

F;1233-1264/Domain: EGF homology <EGF3>

F;1917-1949/Domain: ankyrin repeat homology <AN1>

F;1950-1982/Domain: ankyrin repeat homology <AN2>

F;1984-2016/Domain: ankyrin repeat homology <AN3>

F;2017-2049/Domain: ankyrin repeat homology <AN4>

F;2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match Score 95.5; DB 2; Length 2531;

Best Local Similarity 26.8%; Pred. No. 0.49;

Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

Qy 15 ISACAMILCHGSLQHTPQQHHHLRPEGTCE-VIAHRC-----CNKN 56

Db 679 IDEAGAGSPCH-----NGGTQEDGJAGFTCRCPGSYHDTPLSEVNNECNNS 723

Qy 57 -----RIEBSQTYRKCSLPGKVAGTTRNRPSCYDASIVGKWWCEMPCLGEECKTLP 111

Db 724 PC1HGACRQGLNGYKCDARPG-WSGTNCD-----INNNECESNPVNNGTKDM- 771

Qy 112 DNSWMC 118

Db 772 -TSGTVC 777

RESULT 4

A6019

A;6019 protein - mouse

N;Alternative names: notch protein

C;Species: Mus musculus (house mouse)

C;Accession: S22-Sep-1993 #sequence revision 18-Nov-1994 #text change 07-Mar-2003

C;Accession: A46019; S25144; C49175; B46338; A46488; PM1569; S32109

R;del Amo, F.F.; Genot-Maguire, M.; Jenkins, N.A.; Copeland, N.G.; Grid

Genomics 15, 259-264, 1993

A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of

A;Reference number: A46019; MUID:9319417; PMID:8449489

A;Accession: A46019

A;Status: not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-2331

A;Cross-references: GB:S47228; NID:g288502; PIDN:CAA77941.1; PID:g288503

A;Note: sequence extracted from NCBI backbone (NCBIP:127318)

R;Franco del Amo, F.J.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;

submitted to the EMBL Data Library, April, 1992

A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest

A;Reference number: S25144

A;Accession: S25144

A;Molecule type: mRNA

A;Residues: 1551-2108 'Q', 2110-2114 'ALP', 2118-2170 <ZFA>

A;Cross-references: EMBL:Z11886

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIP:126159)

R;Kopan, R.; Weintraub, H.

J;Cell Biol. 121, 611-614, 1993

A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety o

A;Reference number: A49175; MUID:93178563; PMID:844932

A;Accession: C49175

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1161-1547 <LAR>

A;Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIP:126159)

R;Jardelli, M.; Lendahl, U.

Exp. Cell Res. 204, 364-372, 1993

A;Title: Notch A and Notch B--two mouse Notch homologs correlates with cell fate determinati

A;Reference number: A46438; MUID:93252998; PMID:8486742

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1865-1932 'RR', 1935-1937 'I', 1938-1967 'I', 1969-2044 'IE', 2047-2052 'S', 2054

A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIN:131246; NCBIP:131247)

C;Comment: This protein has many EGF repeats and lin-12(#1172)/Notch repeats.

C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe

C;Genes:

A;Gene: notch-1

A;Map position: 2

A;Note: proximal region of chromosome 2

C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

F;106-138/Domain: EGF homology <EGF1>

F;144-175/Domain: EGF homology <EGF2>

F;222-254/Domain: EGF homology <EGF2>

F;261-292/Domain: EGF homology <EG02>

F;339-370/Domain: EGF homology <EG03>

F;416-449/Domain: EGF homology <EGF3>

F;456-487/Domain: EGF homology <EG04>

F;511-534/Domain: EGF homology <EG05>

F;532-563/Domain: EGF homology <EG06>

F;607-638/Domain: EGF homology <EG07>

F;713-744/Domain: EGF homology <EG08>

F;757-788/Domain: EGF homology <EG09>

F;795-826/Domain: EGF homology <EG10>

F;813-834/Domain: EGF homology <EG11>

F;911-942/Domain: EGF homology <EG12>

F;949-980/Domain: EGF homology <EG13>

F;987-1018/Domain: EGF homology <EG14>

F;1025-1056/Domain: EGF homology <EG15>

F;1063-1094/Domain: EGF homology <EG16>

F:1149-1180/Domain: EGF homology <EG17>
 F:1187-1218/Domain: EGF homology <EG18>
 F:1264/Domain: EGF homology <EGF1>
 F:1352-1383/Domain: EGF homology <EG19>
 F:1391-1425/Domain: EGF homology <EGF2>
 F:1917-1948/Domain: ankyrin repeat homology <AN1>
 F:1949-1981/Domain: ankyrin repeat homology <AN2>
 F:1983-2015/Domain: ankyrin repeat homology <AN3>
 F:2016-2049/Domain: ankyrin repeat homology <AN4>
 F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 95.5; DB 2; Length 2531;
 Best Local Similarity 26.8%; Pred. No. 0.49; Mismatches 7; Indels 51; Gaps 7;
 Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;

Qy 15 ISACAMILCHGSLQHTFQOHHLRPEGGCTC-VIAAHRC-
 Db 679 IDECAAGSPCH-
 Qy 57 ---RIEERSQTVKXCSLPGKVAAGTTRPSCVDASIVGKWCMEPCLEGEBCKTLR 111
 Db 724 PCTHGA CRDGLNGFKCDCAFG-WSGTNCD-
 Qy 112 DNSGWMC 118
 Db 772 -TSGYVC 777

RESULT 5
 T30201 Notch homolog protein - sea squirt (*Halocynthia roretzii*)
 C:Species: *Halocynthia roretzii*
 C:Accession: T30201
 R:Horii, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
 Dev. Genes Evol. 207, 371-380, 1997
 A;Title: Notch homologe from *Halocynthia roretzii* is preferentially expressed in the central nervous system
 A;Reference number: Z30755
 A;Accession: T30201
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: Notch
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.5%; Score 94.5; DB 2; Length 2352;
 Best Local Similarity 26.0%; Pred. No. 0.57; Mismatches 12; Indels 34; Gaps 5;
 Matches 27; Conservative 31; Mismatches 34; Indels 31; Gaps 5;

Qy 32 QOHHLRPEGG-TCEVIAAH-
 Db 236 KRRDLQTEGGFTCNVCYGYGTRDDCSNIDCSNTVACFNARCTDOAGTFCLTPG-- 292

Qy 76 GTTRNRPSC-VDASIVGKWCMEPCLEGEBCKTLPDNSGWMC 118
 Db 293 ---NRILCHDDA-----CISDCARRATCDINPITGSHWMC 325

RESULT 6
 T31070 Notch homolog - sea urchin (*Lyttechinus variegatus*)
 C:Species: *Lyttechinus variegatus* (variegated urchin)
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T31070
 R:Sharwood, D.R.; McClay, D.R.
 Development 124, 3363-3374, 1997
 A;Title: Identification and localisation of a sea urchin Notch homologue: insights into
 A;Reference number: Z20966; PMID:97454256; PMID:9310331
 A;Accession: T31070
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA

A;Residues: 1-2531 <SHE>
 A;Cross-references: EMBL:AF000534; NID:92570350; PID:92570351; PMID:AAA82088-1
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.3%; Score 93; DB 2; Length 2531;
 Best Local Similarity 22.4%; Pred. No. 0.85; Mismatches 18; Indels 38; Gaps 5;
 Matches 28; Conservative 18; Mismatches 41; Indels 38; Gaps 5;

Qy 40 EGTCCEV---TAHRCCNKNRBERGTVKSCLPGKVAGTTRNRSVC-
 Db 350 EGQTCTEINKDDCTPNPQFEGECEDRVASFKCTCPGRTGLLCHLEACMSNPCHTPAQ 409

Qy 86 DASTVIGKWWCMEPCLEG-----FECKTLPD-----NSGMWCA-
 Db 410 STSVVDGSPICDATGGTQGFNCSDIDECISLSMDSTCOSGGTQNFFGWSCLCSSFIG 469

Db 470 SRCT 474

RESULT 7
 A35672 crumbs protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C;Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2003
 C;Accession: A35672
 R:Peppas, U.; Theres, C.; Knust, E.
 Cell 61, 787-799, 1990
 A;Title: crumbs encodes an EGF-like protein expressed on apical membranes of *Drosophila*
 A;Reference number: A35672; PMID:90263104; PMID:2344615
 A;Genetics:

A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: A35672
 A;Status: preliminary
 C:Accession: T30201
 A;Molecule type: protein
 A;Residues: 1-2139 <TEP>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: T30201
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: T30201
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: T30201
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: T30201
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>
 A;Cross-references: EMBL:AB001327; NID:d1024472; PID:d1026501; PMID:BAA25571.1
 C;Genetics:
 A;Gene: FlyBase:crb
 A;Cross-references: FlyBase:FBgn0003688
 C:Keywords: transmembrane protein
 A;Molecule type: mRNA
 A;Residues: 1-2139 <TEP>
 A;Cross-references: GB:M33753
 A;Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue 2007
 A;Accession: T30201
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-2352 <HOB>

RESULT 8
 A24420 notch protein - fruit fly (*Drosophila melanogaster*)
 N;Alternate names: neurogenic repetitive locus protein
 C:Species: *Drosophila melanogaster*
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A24420; AA4768; S09458; A05267
 R:Kidd, S.; Kelley, M.R.; Young, M.W.
 Mol. Cell. Biol. 6, 3094-3108, 1986
 A;Title: Identification and localisation of a sea urchin Notch homologue: insights into
 A;Reference number: A24420
 A;Accession: A24420
 A;Molecule type: DNA
 A;Residues: 1-2703 <KID>

A;Cross-references: GB:K03508; NID:g157991; PID:AA28725.1; PID:g157993
 R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
 Cell 43, 567-581, 1985
 A;Reference number: A24768; MUID:86079539; PMID:3935325
 A;Molecule type: mRNA
 A;Accession: A24768
 A;Residues: 1-48 'I', 50-118 'R', 120-230, 'I', 232-256 'N' 258-266 'A', 268-872 'R', 874-958;
 A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
 R;Wharton, D.
 Nucleic Acids Res. 17, 6463-6471, 1989
 A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
 A;Reference number: S0358; MUID:89385974; PMID:2780284
 A;Accession: S0358
 A;Molecule type: DNA
 A;Residues: 2551-2551, 'QQQQ', 2552-2576, 'E', 2578-2604 <TAU>
 R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
 Cell 40, 55-62, 1985
 A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
 A;Reference number: A05267; MUID:85099329; PMID:2981631
 A;Accession: A05267
 A;Molecule type: DNA
 A;Residues: 2504-2576, 'E', 2578-2611 <WHA2>
 C;Genetics:
 A;Gene: notch; opa
 A;Cross-references: FlyBase:FBgn004647
 A;Mol Position: 8-9, 36
 A;Introns: 53/3, 94/3, 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
 C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C;Keywords: differential tandem repeat; transmembrane protein
 F;27-43:Domain: transmembrane #status predicted <TM1>
 F;29-328:Domain: EGF homology <EGX1>
 F;53-561:Domain: EGF homology <EGF1>
 F;568-599:Domain: EGF homology <EGF2>
 F;988-1019:Domain: EGF homology <EGX2>
 F;1064-1095:Domain: EGF homology <EGF3>
 F;1187-1218:Domain: EGF homology <EGX3>
 F;1746-1762:Domain: transmembrane #status predicted <TM2>
 F;1983-2015:Domain: ankyrin repeat homology <AN1>
 F;1988-2004:Domain: transmembrane #status predicted <TM3>
 F;2050-2082:Domain: ankyrin repeat homology <AN3>
 F;2083-2115:Domain: ankyrin repeat homology <AN4>
 F;2538-2568:Domain: neurogenic repetitive element #status predicted <OPA>
 F;2538-2568:Domain: glutamine-rich

Query Match 11.5%; Score 86.5; DB 1; Length 2703;
 Best Local Similarity 25.9%; Pred. No. 3-9;
 Matches 22; Conservative 10; Mismatches 34; Indels 19; Gaps 3;

Qy 40 EGCECEV---IAAHRCNNKRRIERERSQTWKCSCLPGKVA-----GTRTRRPS 83
 Db 1214 QGQNCELNIDCAPNCPNGGTCHDRVNNSCSCPPGTMGIICEINKDDCKPGACHNNGS 1273
 Qy 84 CYDASITIVGKWNNTEMEPCEGLEEK 108
 Db 1274 CIDR---VGGFFECVCQPGFGVARGC 1295

RESULT 9
 JC7570
 Delta-4 protein - human
 C;Species: Homo sapiens (mar)
 C;Accession: JC7570
 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 16-Aug-2002
 R;Yoneyama, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osaka, M.; Miyatani, S.;
 J. Biochem. 129, 27-34, 2001
 A;Title: Molecular cloning of Delta-4, new mouse and human notch ligand.
 A;Reference number: JC7569; MUID: 21064937; PMID:11334954
 A;Accession: JC7570
 A;Molecule type: mRNA
 A;Residues: 1-685 <YON>
 A;Cross-references: DDBJ:AB043894

RESULT 10
 A;6136
 Jagged protein precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
 C;Accession: A56136
 R;Lindell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
 Cell 80, 909-917, 1995
 A;Title: Jagged: a mammalian ligand that activates Notch1.
 A;Reference number: A56136; MUID:95211842; PMID:7697721
 A;Accession: A56136
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1220 <LIN>
 A;Cross-references: GB:L38483
 F;379-410/Domain: EGF homology <EGF1>
 F;392-423/Domain: EGF homology <EGF2>
 F;634-665/Domain: EGF homology <EGF2>
 Query Match 11.4%; Score 86; DB 2; Length 1220;
 Best Local Similarity 27.0%; Pred. No. 2-1;
 Matches 33; Conservative 9; Mismatches 34; Indels 46; Gaps 9;

Qy 39 PE--GGTCEVIAAHRC---C-NKRNIEERSQTWKCSCLPGKVAGSTRNR----- 81
 Db 326 PEGSGPNCE-TAEHALSLDPHNRSQKETSSGGFEBCSPWTGPCCSTNLDDCSPNNC 384
 Qy 82 ---PSCYDASIVG----KWW-----SG 115
 Db 385 SHGGTCDD-LYNGFKCVCPPWTGKTCQLDANECPKCYNARSCKNLIASYYCDCLPG 442
 Qy 116 WM 117
 Db 443 WM 444

RESULT 11
 A;0136
 fibropellin Ia - sea urchin (Strongylocentrotus purpuratus)
 N;Alternate names: epidermal growth factor homolog precursor
 N;Contains: alternatively spliced fibropellin Ib (EGF1)
 C;Species: Strongylocentrotus purpuratus (purple urchin)
 C;Accession: A40136; B40136; C40136; A29136; A43131
 C;Date: 13-May-1992 #sequence_revision 12-Sep-1997 #text_change 21-Jul-2000
 R;Delgadillo-Reynoso, M.G.; Rollin, D.R.; Hursch, D.A.; Raff, R.A.
 J. Mol. Evol. 29, 314-327, 1989
 A;Title: Structural analysis of the uEGF gene in the sea urchin Strongylocentrotus purpu
 A;Reference number: A40136; MUID:9012459; PMID:2514273
 A;Accession: A40136
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-114
 A;Cross-references: GB:X17530; NID:910225; PID:g667061

A;Accession: B40136
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 181-251; 329-370, 'R', 372-408, 'R', 411-441 <DE2>
A;Accession: C40136
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: K, 747-821, 898-978 <DE3>
A;Reference: Rursh, M.E.; Andrews, R.A.
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'S', 280-481, 786-1064 <HUR>
A;Cross-references: GB:M17421; NID:9161474; PID:9552260
A;R;Hunt, L.C.; Barker, W.C.
FASBB J. 3, 1760-1764, 1989
A;Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A;Reference number: A43131; MUID:3498216; PMID:3498216
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1064 Product: fibropellin I #status predicted <FB>
C;Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F1:1-19/Domain: signal sequence #status predicted <SIG>
F2:2-54/Domain: fibropellin I #status predicted <FB>
F3:2-54/Domain: EGF homology <EG01>
F4:5-175/Domain: Clr/Cls repeat homology <CLR>
F5:10-211/Domain: EGF homology <EG02>
F6:2-8-249/Domain: EGF homology <EG03>
F7:26-287/Domain: EGF homology <EG04>
F8:24-322-363/Domain: EGF homology <EG05>
F9:30-4-401/Domain: EGF homology <EG06>
F10:48-4-439/Domain: EGF homology <EG07>
F11:46-77/Domain: EGF homology <EG08>
F12:48-515/Domain: EGF homology <EG10>
F13:512-553/Domain: EGF homology <EG11>
F14:560-591/Domain: EGF homology <EG12>
F15:598-629/Domain: EGF homology <EG13>
F16:636-667/Domain: EGF homology <EG14>
F17:674-705/Domain: EGF homology <EG15>
F18:712-743/Domain: EGF homology <EG16>
F19:750-781/Domain: EGF homology <EG17>
F20:788-819/Domain: EGF homology <EG18>
F21:826-857/Domain: EGF homology <EG19>
F22:864-895/Domain: EGF homology <EG20>
F23:902-933/Domain: EGF homology <EG21>
F24:936-1064/Region: avdin-like
F25:11-3%; Score 85.5%; DB 2; Length 1064;
Best Local Similarity 28.1%; Pred. No. 2;
Matches 25; Conservative 9; Mismatches 34; Indels 21; Gaps 4;

Qy 40 EGGTCEV---IAAHRCNKRRIEERSQTVKSCCLPGKV--AGTTRNRPSVDASIVG 92
Db 625 EGTNCEINTDEASSPNCMNGGILCDQVNSYVFCLPGFTGIHCIGTE----IDE---- 673
Qy 93 KWCEMPCLPDKNSGWMCATG 121
Db 674 --CASSPCLNLGGQCCTDRVDTSYECVCAG 699

RESULT 12
A;Accession: A35844
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90388285; PMID:2402639
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1254 <COF>
C;Keywords: transmembrane protein; ankyrin repeat homology; EGF homology
C;Comments: Notch protein; ankyrin repeat homology; EGF homology
F:757-788/Domain: EGF homology <EGF3>
F:1025-1056/Domain: EGF homology <EGX1>
F:184-215/Domain: EGF homology <EGF1>
F:222-254/Domain: EGF homology <EGF2>
F:456-487/Domain: EGF homology <EGX2>
F:757-788/Domain: EGF homology <EGF3>
F:1024-1056/Domain: ankyrin repeat homology <AN1>
F:157-198/Domain: ankyrin repeat homology <AN2>
F:1931-2023/Domain: ankyrin repeat homology <AN3>
F:2024-2056/Domain: ankyrin repeat homology <AN4>
F:2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 11.1%; Score 84; DB 2; Length 2524;
Best Local Similarity 23.4%; Pred. No. 6.4%;
Matches 29; Conservative 16; Mismatches 41; Indels 38; Gaps 6;

Qy 23 CHGSQIHTPQQHHLRPEEGTCETV---AHRCCCNKRRIEERS-QTVKSCCLPGKVAG 76
Db 815 CNCMPLPT-----GRAICEAVLAPCAAGSPCKNGRKKESEDFFETSCBPCPGWQGQ 864
Qy 77 T-----T-PRNRPSCVDASITIGRWCMEPCLBS----EBKCTLPDNSGNM 117
Db 865 TCBIDMNECVNPCTNGATCQNTN--GSYKCNCKPGYCSRNCMIDDCQPNFHNGGS 921
Qy 118 CATG 121
Db 922 CSDG 925

RESULT 13
A;Accession: A49175
A;Title: Notch B protein - mouse (fragment)
A;Alternate names: Notch homolog
A;Species: Mus musculus (house mouse)
A;Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 08-Sep-2002
C;Accession: A49175; PMID: 822113
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:143-174/Domain: EGF homology <EGX1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF2>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGX3>

Query Match 10.3%; Score 82.5%; DB 2; Length 1203;
Best Local Similarity 26.4%; Pred. No. 4.5%;
Matches 23; Conservative 11; Mismatches 36; Indels 17; Gaps 4;

Qy 40 EGGTCEV---IAAHRCNKRRIEERSQTVKSCCLPGKVAGTTRNRPS-CVDASIVGK 94

F;1972-2004/Domain: ankyrin repeat homology <AN5>

Db	170	KGVHCELEYNECQSNPCVNNQCVYDKNRFQCLCPPGFTG-----PVCQIDDD-----	218
Qy	95	WCMEPCLEGECKTLPDNSGMATG 121	
Db	219	-CSSTPCLNGAKC1DHPNGYECQQCATG 244	
RESULT 14			
A49128		cell-fate determining gene Notch2 protein - rat	
C;Species:	Rattus norvegicus (Norway rat)		
C;Date:	21-Jun-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002		
C;Accession:	A49128		
R;Weimaster, G.: Roberts, V.J.; Lemke, G.			
D;Development:	116, 931-941, 1992		
A;Title:	Notch2: a second mammalian Notch gene.		
A;Reference number:	A49128; MUID:93202015; PMID:1295745		
A;Accession:	A49128		
A;Status:	preliminary; not compared with conceptual translation		
A;Molecule type:	mRNA		
A;Residues:	1-2471 <WET>		
A;Experimental source:	Schwann cell		
A;Note:	Sequence extracted from NCBI backbone (NCBIP:127811)		
C;Superfamily:	ankyrin repeat homology; EGF homology		
P;264-295/Domain:	EGF homology <EGX1>		
P;79-830/Domain:	EGF homology <EGF1>		
P;877-908/Domain:	EGF homology <EGX2>		
P;1029-1060/Domain:	EGF homology <EGF>		
P;1067-1098/Domain:	EGF homology <EGX3>		
P;1153-1184/Domain:	EGF homology <EGF3>		
P;1191-1222/Domain:	EGF homology <EGX4>		
P;1909-1941/Domain:	ankyrin repeat homology <AN1>		
P;1943-1975/Domain:	ankyrin repeat homology <AN2>		
P;1976-2008/Domain:	ankyrin repeat homology <AN3>		
P;2009-2041/Domain:	ankyrin repeat homology <AN4>		
P;2042-2094/Domain:	ankyrin repeat homology <AN5>		
Query Match			
Qy	40	EGGTCEV-----IAHRCCNKNR1EERSQTVKCSCLPGKVAGTTRNRPSC-VDASIVGKW 94	
Db	487	KGVHCELEYNECQSNPCVNNQCVYDKNRFQCLCPPGFTG-----PVCQIDDD-----	535
Qy	95	WCMEPCLEGECKTLPDNSGMATG 121	
Db	536	-CSSTPCLNGAKC1DHPNGYECQQCATG 561	
RESULT 15			
S45306		notch 3 protein - mouse	
C;Species:	Mus musculus (house mouse)		
C;Date:	20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002		
C;Accession:	S45306		
R;Iardelli, M.; Dahlstrand, J.; Lendahl, U.			
Mech. Dev.	123-136, 1994		
A;Title:	The novel Notch homolog mouse Notch 3 lacks specific epidermal growth factor-		
A;Reference number:	S45306; MUID:95001556; PMID:7918097		
A;Accession:	S45306		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-2318 <LR>		
A;Cross references:	EMBL:X74760; MIG:9483580; PID:CMAS52776.1; PID:9483581		
C;Superfamily:	ankyrin repeat homology; EGF homology		
P;163-195/Domain:	EGF homology <EGF1>		
P;474-505/Domain:	EGF homology <EGF>		
P;854-885/Domain:	EGF homology <EGF2>		
P;1839-1871/Domain:	ankyrin repeat homology <AN1>		
P;1872-1904/Domain:	ankyrin repeat homology <AN2>		
P;1906-1938/Domain:	ankyrin repeat homology <AN3>		
P;1939-1971/Domain:	ankyrin repeat homology <AN4>		

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OM protein - protein search, using sw model

Run on: April 8, 2004, 13:17:35 ; Search time 40 Seconds
(without alignments)
874.269 Million cell updates/sec

Title: US-09-763-335-2

Perfect score: 754

Sequence: 1 MARYSAMSWLYLMISACAM.....SGWMCATGNKIKTRIHPRT 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Published Applications AA:
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 2: /cgm2_6/_ptodata/1/pubpaa/1/pubpaa/_US06_PUBCOMB.pep:
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 15: /cgm2_6/_ptodata/1/pubpaa/1/pubpaa/_US10C_PUBCOMB.pep:
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 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	14.1	3871	15	US-10-369-493-6538
2	106	14.1	3871	15	US-10-369-493-6539
3	95.5	12.7	2531	12	US-10-072-012-470
4	95.5	12.7	2531	12	US-10-072-012-471
5	95.5	12.7	2531	15	US-10-190-115-29
6	95.5	12.7	2531	15	US-10-369-072-29
7	91.5	12.1	233	9	US-03-216-393-110
8	91.5	12.1	233	14	US-10-321-856-110
9	88.5	11.7	2447	15	US-10-190-115-28
10	88.5	11.7	2447	15	US-10-369-072-28
11	87	11.5	188	9	US-09-764-853-773
12	87	11.5	188	9	US-09-764-898-262
13	87	11.5	188	10	US-09-764-881-109
14	87	11.5	188	14	US-10-073-865-88
15	87	11.5	188	15	US-10-242-747-109

%

RESULT 1

US-10-369-493-6538

; Sequence 6538, Application US/10369493

; Publication No. US200302336781

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfang

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-101520522.B

; CURRENT APPLICATION NUMBER: US/10/369-493

; CURRENT FILING DATE: 2003-02-28

; PRIORITY APPLICATION NUMBER: US 60/360,039

; PRIORITY FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO: 6538

; LENGTH: 3871

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6538

Query Match 6538, Score 106; DB 15; Length 3871;

Best Local Similarity 31.2%; Pred. No. 0.15;

Matches 34; Conservative 13; Mismatches 40; Indels 22; Gaps 6;

Qy 24 HGSILQHTFQQLHLHRPPEGTCVIAARCCNKNRIBERSQ-----TVKCSCLPGRVAGT 77

Db 148 HGSL-----CQYHMSAC-SKTFELCPGHCH-LESIVDTGQSSSDTTYKCIICDWFPRVSS 202

Qy 78 TRNRPSCYDADVIGKWCMEBPCLEGKECKLPDN---SGINMCATNK 123

Db 203 DRNPNPTCVDFVN-----ECESNPNCPPGVDCINLPGSSFCVGSG--CPKGK 243

RESULT 2

US-10-369-493-6539
; Sequence 6539, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 3B-10 (52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-18
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; LENGTH: 3871
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; SEQ ID NO: 6539

US-10-369-493-6539
; Sequence 470, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tcherny, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patterson, Meera
; APPLICANT: Shirkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Pastorelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gross, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/255,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517

RESULT 3
US-10-072-012-470
; Sequence 470, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tcherny, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patterson, Meera
; APPLICANT: Shirkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Pastorelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gross, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/255,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517

RESULT 4
US-10-072-012-471
; Sequence 471, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernyev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patterson, Meera
; APPLICANT: Shirkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Pastorelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gross, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/255,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517

Query Match 14.1%; Score 106; DB 15; Length 3871;
Best Local Similarity 31.2%; Pred. No. 0.15; Mismatches 40; Indels 22; Gaps 6;
Matches 34; Conservative 13; Gaps 7;

QY 24 HGSLQHTFOQHHLRPEGCTCEVTAAHRCCKNKRRIERSQ----TYSKSCILPGKVAGT 77
Db 148 HGSL---CQYHNSAC-SKTFELPGPHGHCIESIVDPGQSSDDTTYKICIDWGFKYSS 202

QY 78 TRNRPSCVDAISIVKGKWWCEMPCLEGECKTLPDN--SGNMICATGNK 123
Db 203 DKRNPTCVDN-----ECESNPCHPGVDCINLPGSFVCSG--CPKGYK 243

Query Match 12.7%; Score 95.5; DB 12; Length 2531;
Best Local Similarity 26.8%; Pred. No. 1.2; Mismatches 35; Indels 51; Gaps 7;

QY 15 ISACAMILCHGSLOHTFOQHHLRPEGCTCE-VIAAHRC----CNKN 56
Db 679 IDECAPSPCH-----NGTCDEPGIAGETCRPEGYHDPTCLUSEVNENCSN 723

QY 57 -----REBERSQTVKCCSCLPGVAGTTRNRPSCVDASIVIGKAWCEMPCLEGECKTLP 111
Db 724 PCTHGAARDGLGNGYKCDCAPG-WSGTNCID-----INNNCEENPCVNGGTCDM- 771

QY 112 DNSGMIC 118
Db 772 -TSGYVC 777

PRIOR APPLICATION NUMBER: 60/265,102
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 60/265,514
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,517
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,412
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,395
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/266,406
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 60/266,767
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 60/267,057
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/266,975
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/267,459
 PRIOR FILING DATE: 2001-02-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1391
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 471
 LENGTH: 2531
 TYPE: PRT
 ORGANISM: Rattus norvegicus
 US-10-072-012-471

Query Match 12.7%; Score 95.5; DB 12; Length 2531;
 Best Local Similarity 26.8%; Pred. No. 1.2; Mismatches 7;
 Matches 34; Conservative 7; Indels 51; Gaps 7;

Qy 15 ISACAMILCHGSLOHTPQOHHLARPEGGTE-VIAAHC-
 Db 679 IDCAGSPCH-----NGTCEDTAGFTCRCPGYHDPTCLSEVNECNNSN 723
 Qy 57 ----RIBERSQTVKCSLPGKVAGTTNRPSCVDASTIVGKWCMEBPCLEGEBCKTLP 111
 Db 724 PCTHGAORDGLNGYKDCAPG-WSGTNCD-----INNNECESNPVCVNGGTCKDM- 771

Qy 112 DNSGMIC 118
 Db 772 -TSGYVC 777

RESULT 5
 US-10-190-115-29
 Sequence 29, Application US/10190115
 Publication No. US20030207394A1
 GENERAL INFORMATION:
 ; APPLICANT: Alsobrook, John P. II
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Gross, William M.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Ji, Weizhen
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Nezick, Amanda J.
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shen, Lei
 ; APPLICANT: Shenvy, Suresh G.
 ; APPLICANT: Shimkers, Richard A.
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Szekeres, Edward S. Jr.
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Zerhusen, Bryan D.

RESULT 6
 US-10-369-072-29
 Sequence 29, Application US/10369072
 Publication No. US2004001408A1
 GENERAL INFORMATION:
 ; APPLICANT: Alsobrook II, John P.
 ; APPLICANT: Spaderna, Stephen K.
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Shen, Lei
 ; APPLICANT: Shenvy, Suresh G.
 ; APPLICANT: Shimkers, Richard A.
 ; APPLICANT: Spaderna, Steven K.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Szekeres, Edward S.
 ; APPLICANT: Shenvy, Lei
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Richard
 ; APPLICANT: Shimkets, Richard
 ; APPLICANT: Padigaru, Muralidhara

Page 4

TITLE OF INVENTION: No. US2004001081A1 *Proteins and Nucleic Acids Encoding Same*
FILE REFERENCE: 214-02-050 CON2
CURRENT APPLICATION NUMBER: US10/369,072
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/898,904
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 25331
TYPE: PRT
ORGANISM: Rattus norvegicus

```

Query Match          12.7%; Score 95.5; DB 15; Length 253;
Best Local Similarity 26.8%; Pred. No. 1.2;
Matches 34; Conservative 7; Mismatches 35; Indels 51; Gaps 7;
;

15 ISACAMLLCHGSLQHTFOOHHHLRPEGGTCE-VIAHRC------CNKN 56
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
679 1DEBAGSPPH------NGGTCEDGJAGFTCRPEGYHDPTCLSEVNECSN 723
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
57 ----RIBERSOTYKSCSCLPGKVAGTTTRNRPSCYDASIVIGKWNCEMPCLEGRECKTLP 111
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
724 PCTHGACRGLNGTRCDGAP-WGSTNCID-----INNNCEESNPVNGTCKDM- 771
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
;

112 DNSGWMC 118
| | | | | | | | | | | | | | | | | | | | | | | | | | |
772 -TSGXVC 777
| | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-09-216-393-110
Sequence 110, Application US/09216393
Patent No. US2001001447A1
GENERAL INFORMATION:
APPLICANT: Mihhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
TITTLE OF INVENTION: USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/94,825
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 110
LENGTH: 233
TYPE: PRT
ORGANISM: Toxoplasma gondii

Query Match          12.1%; Score 91.5; DB 9; Length 233;
Best Local Similarity 25.9%; Pred. No. 0.23;
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```

Matches 28; Conservative 6; Mismatches 39; Indels 35; Gaps 4;
Qy      18 CAMLICHGSQHTFQOHHHLRPEGGTCEVIAAHRC-----CNKN---RIEERS 62
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      78 CQCDAHG-----GKCEITKEHCINDSDCNGHCTCINTSNNTNCAGF 122
Qy      63 QTVKCCSLPGKVAGTTRNRPSCVDASIVGKWKWCEMPCLEGEECKTL 110
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      123 AGTNCSSEGGCSGK-----CLSGHCNPATGACYCDPCHGERCETL 165

RESULT 8
US-10-321-856-110
; Sequence 110, Application US/10321856
; Publication No. US20030194393A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USE THEREOF
; FILE REFERENCE: TX-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/321,856
; PRIORITY FILING DATE: 2002-12-17
; PRIORITY APPLICATION NUMBER: 09/216,393
; PRIORITY FILING DATE: 1998-12-18
; PRIORITY APPLICATION NUMBER: 08/994,825
; PRIORITY FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 110
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
; US-10-321-856-110

Query Match Score 91.5; DB 14; Length 233;
Best Local Similarity 25.9%; Pred. No. 0.23;
Matches 28; Conservative 6; Mismatches 39; Indels 35; Gaps 4;
Qy      18 CAMLICHGSQHTFQOHHHLRPEGGTCEVIAAHRC-----CNKN---RIEERS 62
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      78 CQCDAHG-----GKCEITKEHCINDSDCNGHCTCINTSNNTNCAGF 122
Qy      63 QTVKCCSLPGKVAGTTRNRPSCVDASIVGKWKWCEMPCLEGEECKTL 110
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      123 AGTNCSSEGGCSGK-----CLSGHCNPATGACYCDPCHGERCETL 165

```

RESULT 9
US-10-190-115-28
Sequence 28, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alborzbrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Gross, William M.
; APPLICANT: Gussev, Vladimir Y.
; APPLICANT: Jui, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiochong
; APPLICANT: Mezik, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shan, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shmikets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spyrek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zschusen, Bernhard D.

APPLICANT: Voss, Edward Z.
 TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 21402-050 CIP
 CURRENT APPLICATION NUMBER: US/10/190,115
 CURRENT FILING DATE: 2003-02-10
 PRIOR APPLICATION NUMBER: 60/303,168
 PRIOR FILING DATE: 2001-07-05
 PRIOR APPLICATION NUMBER: 60/368,996
 PRIOR FILING DATE: 2000-04-01
 PRIOR APPLICATION NUMBER: 60/386,816
 PRIOR FILING DATE: 2002-06-07
 PRIOR APPLICATION NUMBER: 60/215,854
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,856
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/215,902
 PRIOR FILING DATE: 2000-07-03
 PRIOR APPLICATION NUMBER: 60/216,585
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,586
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/216,722
 PRIOR FILING DATE: 2000-07-07
 PRIOR APPLICATION NUMBER: 60/218,622
 PRIOR FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 60/218,992
 PRIOR FILING DATE: 2000-07-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 136
 SOFTWARE: OurSeqList version 0.1
 SEQ ID NO: 28
 LENGTH: 2447
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-190-115-28

Query Match 11.7%; Score 88.5; DB 15; Length 2447;
 Best Local Similarity 25.4%; Pred. No. 5.9;
 Matches 30; Conservative 10; Mismatches 39; Indels 39; Gaps 5;

Qy 41 GGTCTE---VIAAHRCNCNRRIBERSQTVKCSCLPGKVAGT-----
 Db 404 GPRCEQDYNECASNPQNQTCLDRIGDSICMPG-FGGTH-BENELNBCLSSPCLNRGK 462

Qy 84 CYDASIVIGKWWCE-----
 Db 463 CLDQ---VSRFVCCECPAGFSGEMCQIIDECSCSSTPCNGAKCTIDLPNGYDCBAAEGFK 517

RESULT 11
 US-09-764-853-773
 Sequence 773, Application US/09764853
 Patent No. US20020090672A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 FILE REFERENCE: P0706
 CURRENT APPLICATION NUMBER: US/09/764,853
 CURRENT FILING DATE: 2001-01-17
 Prior application data removed - consult PALM or file wrapper
 NUMBER OF SEQ ID NOS: 939
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 773
 LENGTH: 188
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (97)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (187)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (188)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-764-853-773

RESULT 10
 US-10-369-072-28
 Publication No. US20040014081A1
 GENERAL INFORMATION:
 APPLICANT: Alisbrook II, John P
 APPLICANT: Spadera, Stephen K
 APPLICANT: Tchernev, Velizar
 APPLICANT: Liu, Xiaohong
 APPLICANT: Shanyo, Suresh
 APPLICANT: Spytek, Kimberly
 APPLICANT: Zerhusen, Bryan
 APPLICANT: Patturajan, Meera
 APPLICANT: Taupier, Raymond T
 APPLICANT: Rastelli, Luca
 APPLICANT: Gross, William M
 APPLICANT: Sperkeres, Edward S
 APPLICANT: Lepley, Denise M
 APPLICANT: Shen, Lei
 APPLICANT: Burgess, Catherine E
 APPLICANT: Shimkets, Richard
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Title of Invention: No. US2004001081A1
 FILE REFERENCE: 21402-050 CON2
 CURRENT APPLICATION NUMBER: US/10/369,072
 CURRENT FILING DATE: 2003-02-18

Query Match 11.5%; Score 87; DB 9; Length 188;
 Best Local Similarity 25.0%; Pred. No. 0.53;

CURRENT FILING DATE: 2002-09-13
 PRIOR APPLICATION NUMBER: 09/764,881
 PRIOR FILING DATE: 2001-01-17
 PRIOR APPLICATION NUMBER: 60/179,065
 PRIOR FILING DATE: 2000-01-31
 PRIOR APPLICATION NUMBER: 60/180,628
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: 60/214,886
 PRIOR FILING DATE: 2000-06-28
 PRIOR APPLICATION NUMBER: 60/217,487
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,758
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/220,963
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: 60/217,496
 PRIOR FILING DATE: 2000-07-11
 PRIOR APPLICATION NUMBER: 60/225,447
 PRIOR FILING DATE: 2000-08-14
 PRIOR APPLICATION NUMBER: 60/218,290
 PRIOR FILING DATE: 2000-07-14
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 192
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 109
 LENGTH: 188
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (97)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (187)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (187)
 OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
 US-10-242-747-109

Query Match 11.5%; Score 87; DB 15; Length 188;
 Best Local Similarity 25.0%; Pred. No. 0.53;
 Matches 28; Conservative 9; Mismatches 45; Indels 30; Gaps 6;
 Qy 14 WISAC---AMLLCHGSLOHTFQDHLHRPEGGTCEVIAAHRCNNKRIERSOTVKSC 69
 Db 18 WQCTCDEGNGLFDQDLYNC--THASPKNGATC-----SNSGQRSYT--CTC 62
 Qy 70 LPGRKVAGTTTRNRPSCVDASIVIGKWWCMEPLGECKTLPDNSGMNCATG 121
 Db 63 RPYGTG-----VDCBLELSE--CDSNPCCRNGGSKDQEDGYXCLCPG 103

Search completed: April 8, 2004, 13:23:16
 Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: April 8, 2004, 13:14:59 ; Search time 39 Seconds

(without alignment)
1075.998 Million cell updates/sec

Title: US-09-763-335-2

Perfect score: 754

Sequence: 1 MAMYSAMSWLYLMSACAM.....SGWMCATGNKIKTRIHPRT 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL_25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacterioplasm:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	Q7Z5A9	2	133	11	Q7TPG8	Q7Z5A9 homo sapien
2	Q7Z5A9	2	133	11	Q7TPG8	Q7TPG8 mus musculu
3	Q7Z5A9	2	133	4	Q8TC18	Q8TC18 homo sapien
4	Q7Z5A9	2	135	11	Q7TPG5	Q7TPG5 mus musculu
5	Q7Z5A9	2	140	6	Q9nOD3	Q9nOD3 macaca fasc
6	Q7Z5A9	2	140	4	Q96LR4	Q96LR4 homo sapien
7	Q7Z5A9	2	140	6	Q95k92	Q95k92 macaca fasc
8	Q7Z5A9	2	131	4	Q8N3H0	Q8N3H0 homo sapien
9	Q7Z5A9	2	132	11	Q7TPG6	Q7TPG6 mus musculu
10	Q7Z5A9	2	131	11	Q7TPG7	Q7TPG7 mus musculu
11	Q7Z5A9	2	126	11	Q8BV02	Q8BV02 mus musculu
12	Q7Z5A9	2	133	4	Q7Z5A8	Q7Z5A8 homo sapien
13	Q7Z5A9	2	125	4	Q7TPG7	Q7TPG7 homo sapien
14	Q7Z5A9	2	125	11	Q91WE9	Q91WE9 mus musculu
15	Q7Z5A9	2	132	4	Q8IXR8	Q8IXR8 homo sapien
16	Q7Z5A9	2	132	11	Q8C1V6	Q8C1V6 mus musculu

RESULT 2
Q7TPG8

SEQUENCE FROM N.A.
Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;
"TAFA: A Novel Secreted Family with Homology to CC-chemokines.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY323114; AAP2406.1; -
SEQUENCE 133 AA; 14901 MW; C5DD1C7E5F997386 CRC64;

Query Match 100.0%; Score 754; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;
"TAFA: A Novel Secreted Family with Homology to CC-chemokines.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY323114; AAP2406.1; -
SEQUENCE 133 AA; 14901 MW; C5DD1C7E5F997386 CRC64;

RESULT 1
Q7Z5A9
ID Q7Z5A9 PRELIMINARY; PRT; 133 AA.
AC Q7Z5A9; DT 01-OCT-2003 (TREMBLrel. 25, Created); DR 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE TAFAL-
OS Homo sapiens (Human)
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TAXID:9606; OX [1]
RN SEQUENCE FROM N.A.
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;
"TAFA: A Novel Secreted Family with Homology to CC-chemokines.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY323114; AAP2406.1; -
SEQUENCE 133 AA; 14901 MW; C5DD1C7E5F997386 CRC64;

Query Match 100.0%; Score 754; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.6e-80;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAMVSAMSWLYLWISACAMLCHGSLSQTFQOHILHRPEGTCTEVIAAHRCCKNKR1EE 60
Db 1 MAMVSAMSWLYLWISACAMLCHGSLSQTFQOHILHRPEGTCTEVIAAHRCCKNKR1EE 60
OY 61 RSQTVCSCSLPGKVACTRNPSCVDASIVGKWCMEPCLEGECKTLPDNSGMAT 120
Db 61 RSQTVCSCSLPGKVACTRNPSCVDASIVGKWCMEPCLEGECKTLPDNSGMAT 120
OY 121 GNKIKTRIHR1 133
Db 121 GNKIKTRIHR1 133

Db	78 CPPGQVACTTRAGPSCYEA TIVTQKWNCHMNPCLGECKVLPDYSSWCSGGNKVTTK	137	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; OC Cercopithecinae; Macaca. OX NCBI_TAXID=9541; RN [1] RP SEQUENCE FROM N.A. RC TISSUE-Medulla oblongata; RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., RA Suzuki Y., Sugano S., Hashimoto K.; RA "Isolation of full-length cDNA clones from macaque brain cDNA libraries"; RR Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases DR AB061062; BAB60184.; -. KW Hypothetical protein. SQ SEQUENCE 140 AA; 15654 MW; 17324670B6C97E19 CRC64; Query Match 57.7%; Score 435; DB 6; Length 140; Best Local Similarity 62.0%; Pred. No. 6 1e-43; Matches 75; Conservative 15; Mismatches 31; Indels 0; Gaps 0;
RESULT 6			
Db	Q96LR4 ID Q96LR4; PRELIMINARY;	140 AA.	QY RN 129 I 129 Db 138 V 138
AC	Q96LR4; DT 01-DEC-2001 (TREMBLrel. 19, Created)		
DT	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein FLJ25161 (Similar to expressed sequence AW045604) (TAFA4).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TAXID=9606;		
[1]	BN PRELIMINARY;		
RP SEQUENCE FROM N.A.			
RC TISSUE-Brain;			
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., RA Fujimori Y., Komiyama M., Kawamura M., Hata H., RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T., RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., RA Nagai K., Isogai T., Sugano S.;			
RT "NEDO human cDNA sequencing Project.";			
RT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.			
[2]	BN PRELIMINARY;		
RP SEQUENCE FROM N.A.			
RA Strausberg R.;			
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.			
[3]	RP SEQUENCE FROM N.A.		
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.			
DR EMBL; AK057890; BAB71606.1; -.			
DR EMBL; BC031166; AAH31166.1; -.			
DR EMBL; AY325117; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 140 AA; 15682 MW; 173254FBBS26009 CRC64;			
Query Match 57.9%; Score 436.5; DB 4; Length 140;			
Best Local Similarity 61.1%; Pred. No. 4e-43;			
Matches 80; Conservative 16; Mismatches 30; Indels 5; Gaps 2;			
QY RN 119 ATGNKIXTKTRI 129 Db 128 SSGNKVKTTKV 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
RESULT 7			
Db	Q95K92 ID Q95K92; PRELIMINARY;	140 AA.	
AC	Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)		
DT	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein.		
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
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AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
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RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
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KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
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AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			
RN [1]	SEQUENCE FROM N.A.		
RP SEQUENCE FROM N.A.			
RC TISSUE-Amygdala;			
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.;			
RT "TAFA: A Novel Family with Homology to CC-chemokines.";			
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases			
DR EMBL; AL834160; CAD38165.1; -.			
DR EMBL; AY325115; AAP92409.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 131 AA; 14620 MW; 6D7EDDB2B59965F4 CRC64;			
Query Match 57.3%; Score 432; DB 4; Length 131;			
Best Local Similarity 61.2%; Pred. No. 1.3e-12;			
Matches 74; Conservative 14; Mismatches 23; Indels 10; Gaps 1;			
QY RN 129 ATGNKIXTKTRI 129 Db 138 V 138			
AC Q95K92; DT 01-DEC-2001 (TREMBLrel. 19, Created)			
DT 01-OCT-2003 (TREMBLrel. 19, Last sequence update)			
DE Hypothetical protein.			
OS			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TAXID=9606;			

Qy	129 I 129	Db	129 V 129	Db	69 CFPGQVAGTTRAPSCVDASIVQKWWCEMPCLEBECKVLPDKKGWSSSGNKVKTR 128
RESULT 9					
Q7TPG6	ID Q7TPG6; PRELIMINARY; PRT; 132 AA.	Q7TPG6	ID Q7TPG6; PRELIMINARY; PRT; 132 AA.	Q7TPG6	ID Q7TPG6; PRELIMINARY; PRT; 132 AA.
AC Q7TPG6;		AC Q7TPG6;		AC Q7TPG6;	
DT 01-OCT-2003 (TREMBLrel. 25, Created)		DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)		DT 01-MAR-2003 (TREMBLrel. 23, Created)	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE TAFAP3.		DE TAFAP3.		DE TAFAP3.	
OS Mus musculus (Mouse).		OS Mus musculus (Mouse).		OS Mus musculus (Mouse).	
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;		NCBI_TaxID=10090;		NCBI_TaxID=10090;	
RN [1]		RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=57BL/6J;		RC STRAIN=57BL/6J;		RC STRAIN=C57BL/6J;	
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";		RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";		RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";	
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.	
DR EMBL:AY325122; AAP92414.1; -		DR EMBL:AY325122; AAP92414.1; -		DR EMBL:AY325122; AAP92414.1; -	
SQ SEQUENCE 132 AA; 14426 MW; 2D60C5AE1BA3F00 CRC64;		SQ SEQUENCE 132 AA; 14426 MW; 2D60C5AE1BA3F00 CRC64;		SQ SEQUENCE 126 AA; 13975 MW; D2AA1F362D44ACBA CRC64;	
Query Match 57.0%; Score 429 5; DB 11; Length 132; Best Local Similarity 61.5%; Pred. No. 2.5e-42; Matches 83; Conservative 13; Mismatches 16; Indels 23; Gaps 4;		Query Match 55.0%; Score 415; DB 11; Length 126; Best Local Similarity 62.9%; Pred. No. 1.2e-40; Matches 73; Conservative 14; Mismatches 25; Indels 4; Gaps 2;		Query Match 55.0%; Score 415; DB 11; Length 126; Best Local Similarity 62.9%; Pred. No. 1.2e-40; Matches 73; Conservative 14; Mismatches 25; Indels 4; Gaps 2;	
Qy 5 SAMSWLXL--WISACAMLCHGSLSQHTPQQHHLHRP-----EGTCVTAAHCCN 54		Qy 5 SAMSWLXL--WISACAMLCHGSLSQHTPQQHHLHRP-----EGTCVTAAHCCN 54		Qy 5 SAMSWLXL--WISACAMLCHGSLSQHTPQQHHLHRP-----EGTCVTAAHCCN 54	
Db 9 SAGSWSVIALCLAVLWLWTCP--ASASLQ-----BPTSAVNLVKQGTCTVIAHCCN 55		Db 9 SAGSWSVIALCLAVLWLWTCP--ASASLQ-----BPTSAVNLVKQGTCTVIAHCCN 55		Db 9 WLYLWISACAMLCHGSLSQHTPQQHHLHRP-----EGTCVTAAHCCN 55	
Qy 55 KNRLEERQTQVSCLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKLDPNS 114		Qy 55 KNRLEERQTQVSCLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKLDPNS 114		Qy 55 KNRLEERQTQVSCLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKLDPNS 114	
Db 56 RNRLEERSTQVKCSCLSGQAVGTRAKPSQDASIVQKWWCQMEPCLLGECKVLPDLS 115		Db 56 RNRLEERSTQVKCSCLSGQAVGTRAKPSQDASIVQKWWCQMEPCLLGECKVLPDLS 115		Db 56 RNRLEERSTQVKCSCLSGQAVGTRAKPSQDASIVQKWWCQMEPCLLGECKVLPDLS 115	
Qy 115 GMCATGNKIKTRI 129		Qy 115 GMCATGNKIKTRI 129		Qy 115 GMCATGNKIKTRI 129	
Db 116 GWSSSSGHKVKTRIKV 130		Db 116 GWSSSSGHKVKTRIKV 130		Db 116 GWSSSSGHKVKTRIKV 130	
RESULT 10		RESULT 10		RESULT 10	
Q7TPG7	ID Q7TPG7; PRELIMINARY; PRT; 131 AA.	Q7TPG7	ID Q7TPG7; PRELIMINARY; PRT; 131 AA.	Q7TPG7	ID Q7TPG7; PRELIMINARY; PRT; 131 AA.
AC Q7TPG7;		AC Q7TPG7;		AC Q7TPG7;	
DT 01-OCT-2003 (TREMBLrel. 25, Created)		DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)		DT 01-OCT-2003 (TREMBLrel. 25, Created)	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)		DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)	
DE TAFAP2.		DE TAFAP2.		DE TAFAP2.	
OS Mus musculus (Mouse).		OS Mus musculus (Mouse).		OS Mus musculus (Mouse).	
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI_TaxID=10090;		NCBI_TaxID=10090;		NCBI_TaxID=10090;	
RN [1]		RN [1]		RN [1]	
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC STRAIN=57BL/6J;		RC STRAIN=57BL/6J;		RC STRAIN=57BL/6J;	
RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";		RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";		RA Tang Y.T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F.; RT "TAFAP: A Novel Secreted Family with Homology to C-C-chemokines.";	
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.		RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.	
SQ SEQUENCE 131 AA; 14647 MW; FE70D61916A95F47 CRC64;		SQ SEQUENCE 131 AA; 14647 MW; FE70D61916A95F47 CRC64;		SQ SEQUENCE 131 AA; 14647 MW; FE70D61916A95F47 CRC64;	
Query Match 56.9%; Score 429; DB 11; Length 131; Best Local Similarity 61.2%; Pred. No. 2.8e-42; Matches 74; Conservative 12; Mismatches 25; Indels 10; Gaps 1;		Query Match 56.9%; Score 429; DB 11; Length 131; Best Local Similarity 61.2%; Pred. No. 2.8e-42; Matches 74; Conservative 12; Mismatches 25; Indels 10; Gaps 1;		Query Match 56.9%; Score 429; DB 11; Length 131; Best Local Similarity 61.2%; Pred. No. 2.8e-42; Matches 74; Conservative 12; Mismatches 25; Indels 10; Gaps 1;	
Qy 9 WVLYLWISACAMLCHGSLSQHTPQQHHLHRPEGCTVIAHCCNKORIEBRSQTVKCS 68		Qy 9 WVLYLWISACAMLCHGSLSQHTPQQHHLHRPEGCTVIAHCCNKORIEBRSQTVKCS 68		Qy 9 WVLYLWISACAMLCHGSLSQHTPQQHHLHRPEGCTVIAHCCNKORIEBRSQTVKCS 68	
Db 19 FIVTLW-----GXAVSSANHHKAHHVRGTCVEVLAHRCCNQNKEERSQTVKCS 68		Db 19 FIVTLW-----GXAVSSANHHKAHHVRGTCVEVLAHRCCNQNKEERSQTVKCS 68		Db 19 FIVTLW-----GXAVSSANHHKAHHVRGTCVEVLAHRCCNQNKEERSQTVKCS 68	
Qy 69 CLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKVLPDNSGMATGNKIKTR 128		Qy 69 CLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKVLPDNSGMATGNKIKTR 128		Qy 69 CLPGKVAGTTRNPSCVDASIVQKWWCEMPCLEBECKVLPDNSGMATGNKIKTR 128	

Db	10	STGGWLLAICLAWLWTHLTAALQPTATVLVQQ-----GTCEVIAAHRCNNRNRLE	61	DR EMBL; AY325124; AAP92416.1; -.
Qy	60	ERSQTVKCSCLPGRKAGTTRNPSCVDASIVIGRWCMEPCBLEBECKTLPLDNGWMCA	119	MGD; MGI:2146182; AW041604.
Db	62	ERSQTVKCSCLFSGQVAGTTRAKPSCVDASIVLQRMWCOMEPCLFGEECKVLPLDLSGWSCS	121	KW Hypothetical protein.
Qy	120	TGNKIKTRTRI 129	125;	SQ SEQUENCE 125 AA; 13592 MW; A8BCA8D09F86404A CRC64 ;
Db	122	SGHKVKTIVY 131	3;	Query Match 32.8%; Score 247.5; DB 11; Length 125;
RESULT 13				
Db	Q725A7	PRELIMINARY;	PRT; 125 AA.	Best Local Similarity 44.3%; Pred. No. 4.7e-21;
AC	Q725A7			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
DT	01-OCT-2003	(TREMBrel. 25, Created)		Query Match 32.8%; Score 247.5; DB 11;
DT	01-OCT-2003	(TREMBrel. 25, Last sequence update)		Best Local Similarity 44.3%; Pred. No. 4.7e-21;
DE		(TREMBrel. 25, Last annotation update)		Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
OS	Homo sapiens (Human).			Query Match 32.8%; Score 247.5; DB 11;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			Best Local Similarity 44.3%; Pred. No. 4.7e-21;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
OX	NCBI_TaxID=9606;			Query Match 32.8%; Score 247.5; DB 4; Length 125;
RN		SEQUENCE FROM N.A.		Best Local Similarity 44.3%; Pred. No. 4.7e-21;
RA	Tang Y. T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F. ;			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
RT	"TAFa: A Novel Secreted Family with Homology to C-CheMokines."			Query Match 32.8%; Score 247.5; DB 4; Length 125;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			Best Local Similarity 44.3%; Pred. No. 4.7e-21;
DR	AY325118; AAF92410.1; -			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
SQ	SEQUENCE 125 AA; 13592 MW; A8BCA8D09F86404A CRC64 ;			Query Match 32.8%; Score 247.5; DB 4; Length 125;
RESULT 15				
Db	Q8IXR8	PRELIMINARY;	PRT; 132 AA.	Best Local Similarity 44.3%; Pred. No. 4.7e-21;
AC	Q8IXR8			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
DT	01-MAR-2003	(TREMBrel. 23, Created)		Query Match 32.8%; Score 247.5; DB 4; Length 125;
DT	01-MAR-2003	(TREMBrel. 23, Last sequence update)		Best Local Similarity 44.3%; Pred. No. 4.7e-21;
DT	01-MAR-2003	(TREMBrel. 23, Last annotation update)		Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
OS	Homo sapiens (Human).			Query Match 32.8%; Score 247.5; DB 4; Length 125;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			Best Local Similarity 44.3%; Pred. No. 4.7e-21;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
OX	NCBI_TaxID=9606;			Query Match 32.8%; Score 247.5; DB 4; Length 125;
RN		SEQUENCE FROM N.A.		Best Local Similarity 44.3%; Pred. No. 4.7e-21;
RP		TISSUE:Brain;		Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
RA	Strausberg R.			Query Match 32.8%; Score 247.5; DB 4; Length 125;
RP		SEQUENCE FROM N.A.		Best Local Similarity 44.3%; Pred. No. 4.7e-21;
RA	Strausberg R.			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
DR	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			Query Match 32.8%; Score 247.5; DB 4; Length 125;
DR	EMBL; BC039396; AAH39396.1; -			Best Local Similarity 44.3%; Pred. No. 4.7e-21;
SQ	SEQUENCE 132 AA; 14300 MW; 16BEE9F574FB0066 CRC64 ;			Matches 54; Conservative 14; Mismatches 45; Indels 9; Gaps 3;
RESULT 16				
Qy	13	LWISACAMILCHGSILQHTFQOHHLHRPEG----GTCEVIAAHRCNNRNRLE	68	DR EMBL; BC039396; AAH39396.1; -
Db	7	LWALAGAAALCCFLVL---VTHAQFLKECQLQAAGTCETVLDRDSSQPRTRARCARCA	62	KCSCLPKGAVGTRNRSQCVDAASIVIGRWCMEPCBLEGECKTLPLDNGWMCA-TGNKIKTRI 124
Qy	69	CIGKVGATTRNRSQCVDAASIVIGRWCMEPCBLEGECKTLPLDNGWMCA-TGNKIKTRI 127	124;	66 QLAAGTCETVLDRDSQPRTRARCARCA
Db	63	CRKQIAQGTRARPACVDARIKTKQWCDMLPCLGEGCCDLINRSGWTCQFGRIKTT 122	126	67 RCACRKQGIAQGTRARPACVDARIKTKQWCDMLPCLGEGCCDLINRSGWTCQFGRIKTT 126
Qy	128	RI 129	129;	725 KTRTRI 129
Db	123	TV 124	124;	127 KTTTV 131
RESULT 17				
Q1WE9	Q1WE9	PRELIMINARY;	PRT; 125 AA.	Search completed: April 8, 2004, 13:17:32
AC	Q1WE9			Job time : 40 secs
DT	01-DEC-2001	(TREMBrel. 19, Created)		
DT	01-DEC-2001	(TREMBrel. 19, Last sequence update)		
DT	01-OCT-2003	(TREMBrel. 25, Last annotation update)		
DE		Hypothetical protein (TAFaS).		
GN	AW049604.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=57BL/6J;			
RA	Tang Y. T., Emtage P., Funk W., Hu T., Arterburn M., Park E., Rupp F. ;			
RT	"TAFa: A Novel Secreted Family with Homology to C-CheMokines."			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC015306; AAH15306.1; -			